



sequence listing_ST25.txt
SEQUENCE LISTING

<110> Japan Science and Technology Agency
Kuroda, Shunichi
Tanizawa, Katsuyuki
Okajima, Toshihide
Kondo, Akihiko
Ueda, Nasakazu
Seno, Masahura

<120> THERAPEUTIC DRUG USING ANTIBODY-DISPLAYING HOLLOW PROTEIN
NANOPARTICLES AND HOLLOW PROTEIN NANOPARTICLES

<130> 12480-000067/US

<150> 10/509,249

<151> 2004-09-28

<160> 245

<170> PatentIn version 3.4

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sequence listing_ST25.txt

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sequence listing_ST25.txt

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<212> PRT
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<220>
<223> artificial synthesized peptide sequence

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<210> 29
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<212> PRT
<213> artificial sequence

<220>
<223> artificial synthesized peptide sequence

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1 5 10 15

Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln
20 25 30

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Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala
35 40 45

Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn
50 55 60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65 70 75 80

Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro
85 90 95

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<400> 30
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<210> 31
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<212> DNA
<213> Artificial Sequence Fused Peptide

<220>
<223> 21-153 + ZZ (serotype y) sequence

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gctgctgctg ctgctgctag aagaagaaga agaagaaga 39

<210> 32
<211> 378
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<213> artificial sequence

<220>
<223> protein corresponding to 21-153 + ZZ (serotype y) sequence

<400> 32

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
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His Gln Leu Asp Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn
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20

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Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser
275 280 285

Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile
290 295 300

Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val
305 310 315 320

Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val
325 330 335

Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr
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Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu
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Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
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<210> 33
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<212> DNA
<213> artificial sequence

<220>
<223> 21-153 (Q129R) + ZZ (serotype y) sequence

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tatgagatct tacatttacc taacttaaac gaagaacaac gaaacgcctt catccaaagt 360
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tgtattccca tcccatcatc ctgggctttc gcaagattcc tatgggagtg ggcctcagtc      960
cgtttctcct ggctcagttt actagtgcc a tttgttcagt ggttcgtagg gctttccccc    1020
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<210> 34
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 <213> artificial sequence

<220>
 <223> Protein corresponding to 21-153 (Q129R) + ZZ (serotype y)
 sequence

<400> 34

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn
 20 25 30

Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
 35 40 45

Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys
 50 55 60

Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu
 65 70 75 80

Asn Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln
 85 90 95

Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu
 100 105 110

Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser
 115 120 125

Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro
 130 135 140

Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe
 145 150 155 160

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Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg
165 170 175

Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn
180 185 190

Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro
195 200 205

Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
210 215 220

Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu
225 230 235 240

Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu
245 250 255

Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro
260 265 270

Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser
275 280 285

Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile
290 295 300

Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val
305 310 315 320

Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val
325 330 335

Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr
340 345 350

Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu
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Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
370 375

<210> 35

<211> 1134

<212> DNA

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sequence listing_ST25.txt

<223> 21-153 (G145R) + ZZ (serotype y) sequence

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<210> 36

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<223> Protein corresponding to 21-153 (G145R) + ZZ (serotype y) sequence

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His Gln Leu Asp Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn
20 25 30

Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
35 40 45

sequence listing_ST25.txt

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Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys
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Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu
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Asn Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln
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Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu
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Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser
      115         120         125

Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro
      130         135         140

Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe
145          150         155         160

Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg
      165         170         175

Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn
      180         185         190

Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro
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Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
      210         215         220

Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu
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Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu
      245         250         255

Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro
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Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser
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Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile

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Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val
325 330 335

Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr
340 345 350

Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu
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Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
370 375

<210> 37
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<223> 21-153 (Q129R/G145R) + ZZ-tag (serotype y) sequence

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<223> Protein corresponding to 21-153 (Q129R/G145R) + ZZ-tag (serotype y) sequence

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Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
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His Gln Leu Asp Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn
20 25 30

Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
35 40 45

Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys
50 55 60

Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu
65 70 75 80

Asn Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln
85 90 95

Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu
100 105 110

Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser
115 120 125

Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro
130 135 140

Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe
145 150 155 160

Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg
165 170 175

sequence listing_ST25.txt

Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn
180 185 190

Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro
195 200 205

Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
210 215 220

Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu
225 230 235 240

Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu
245 250 255

Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro
260 265 270

Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser
275 280 285

Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile
290 295 300

Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val
305 310 315 320

Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val
325 330 335

Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr
340 345 350

Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu
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Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
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<210> 39
<211> 933
<212> DNA
<213> artificial sequence

<220>
<223> 21-153 + EGF (serotype y) sequence

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sequence listing_ST25.txt

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<210> 40

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<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 21-153 + EGF (serotype y) sequence

<400> 40

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu
20 25 30

Ser His Asp Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu
35 40 45

Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu
50 55 60

Arg Cys Gln Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala
65 70 75 80

Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
85 90 95

sequence listing_ST25.txt

```

Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
      100      105      110

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
      115      120      125

Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
      130      135      140

His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
      145      150      155      160

Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
      165      170      175

Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
      180      185      190

Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
      195      200      205

Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
      210      215      220

Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
      225      230      235      240

Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
      245      250      255

Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
      260      265      270

Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
      275      280      285

Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
      290      295      300

Phe Cys Leu Trp Val Tyr Ile
      305      310

```

```

<210> 41
<211> 933
<212> DNA
<213> artificial sequence

```

sequence listing_ST25.txt

<220>

<223> 21-153 (Q129R) + EGF (serotype y) sequence

<400> 41

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atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac    60
ggcggccgca tgaactctga ttccgaatgc ccgctgtctc atgacggtta ctgcctgcat    120
gatggcgtat gcatgtacat cgaagctctg gacaaatacg catgcaactg tgttgtaggt    180
tacatcggcg aacgttgcca gtatcgcgac ctgaaatggt gggaactgcg taaggcggcc    240
gccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta    300
caggcggggg ttttcttggt gacaagaatc ctcaacaata cacagagtct agactcgtgg    360
tggacttctc tcaatcttct agggggagca cccacgtgtc ctggccaaaa ttcgcagtcc    420
ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg    480
tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttggtg    540
gttcttctgg actaccaagg tatgttgccc gtttgtcctc tacttccagg aacatcaacc    600
accagcacgg ggccatgcaa gacctgcacg attcctgctc gaggaacctc tatgtttccc    660
tcttgttgct gtacaaaacc ttcggacgga aactgcactt gtattcccat cccatcatcc    720
tgggctttcg caagattcct atgggagtggt gcctcagtcc gtttctcctg gctcagttta    780
ctagtccat ttgttcagtg gttcgtaggg ctttcccca ctgtttggt ttcagttata    840
tggatgatgt ggtattgggg gccaaagtctg tacaacatct tgagtcctt tttacctcta    900
ttaccaattt tcttttgtct ttgggtatac att                                933
```

<210> 42

<211> 311

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 21-153 (Q129R) + EGF (serotype y) sequence

<400> 42

```
Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10           15
```

```
His Gln Leu Asp Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu
20           25           30
```

```
Ser His Asp Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu
35           40           45
```

```
Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu
50           55           60
```

sequence listing_ST25.txt

Arg Cys Gln Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala
 65 70 75 80
 Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
 85 90 95
 Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
 100 105 110
 Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
 115 120 125
 Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
 130 135 140
 His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
 145 150 155 160
 Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
 165 170 175
 Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
 180 185 190
 Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
 195 200 205
 Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
 210 215 220
 Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
 225 230 235 240
 Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
 245 250 255
 Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
 260 265 270
 Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
 275 280 285
 Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
 290 295 300
 Phe Cys Leu Trp Val Tyr Ile
 305 310

sequence listing_ST25.txt

<210> 43
<211> 933
<212> DNA
<213> artificial sequence

<220>
<223> 21-153 (G145R) + EGF (serotype y) sequence

<400> 43
atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac 60
ggcggccgca tgaactctga ttccgaatgc ccgctgtctc atgacgggta ctgcctgcat 120
gatggcgtat gcatgtacat cgaagctctg gacaaatacg catgcaactg tgttgtaggt 180
tacatcggcg aacgttgcca gtatcgcgac ctgaaatggg ggggaactgcg taaggcggcc 240
gcccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta 300
caggcggggg ttttcttggt gacaagaatc ctcaacaata cacagagtct agactcgtgg 360
tggacttctc tcaattttct agggggagca cccacgtgtc ctggccaaaa ttcgcagtcc 420
ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 480
tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttggtg 540
gttcttctgg actaccaagg tatgttgccc gtttgtcctc tacttccagg aacatcaacc 600
accagcacgg ggccatgcaa gacctgcacg attcctgctc aaggaacctc tatgtttccc 660
tcttgttgct gtacaaaacc ttcggacaga aactgcactt gtattcccat cccatcatcc 720
tgggctttcg caagattcct atgggagtg gctcagtcg gtttctcctg gctcagttta 780
ctagtgccat ttgttcagtg gttcgtaggg ctttcccca ctgtttggct ttcagttata 840
tggatgatgt ggtattgggg gccaaagtctg tacaacatct tgagtcctt tttacctcta 900
ttaccaattt tcttttgtct ttgggtatac att 933

<210> 44
<211> 311
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 21-153 (G145R) + EGF (serotype y) sequence

<400> 44
Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15
His Gln Leu Asp Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu
20 25 30

sequence listing_ST25.txt

Ser His Asp Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu
35 40 45

Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu
50 55 60

Arg Cys Gln Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala
65 70 75 80

Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
85 90 95

Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
100 105 110

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
115 120 125

Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
130 135 140

His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
145 150 155 160

Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
165 170 175

Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
180 185 190

Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
195 200 205

Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
210 215 220

Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
225 230 235 240

Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
245 250 255

Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
260 265 270

Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
275 280 285

sequence listing_ST25.txt

Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
290 295 300

Phe Cys Leu Trp Val Tyr Ile
305 310

<210> 45
<211> 933
<212> DNA
<213> artificial sequence

<220>
<223> 21-153 (Q129R/G145R) + EGF (serotype y) sequence

<400> 45
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ggcggccgca tgaactctga ttccgaatgc ccgctgtctc atgacgggta ctgcctgcat 120
gatggcgtat gcatgtacat cgaagctctg gacaaatacg catgcaactg tggtgtaggt 180
tacatcggcg aacgttgcca gtatcgcgac ctgaaatggg gggaactgcg taaggcggcc 240
gcccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta 300
caggcgggggt ttttcttggt gacaagaatc ctcacaatac cacagagtct agactcgtgg 360
tggaattctc tcaattttct agggggagca cccacgtgtc ctggccaaaa ttcgcagtcc 420
ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 480
tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttggtg 540
gttcttctgg actaccaagg tatgttgccc gtttgcctc tacttccagg aacatcaacc 600
accagcacgg ggccatgcaa gacctgcacg attcctgtc gaggaacctc tatgtttccc 660
tcttggtgct gtacaaaacc ttcggacaga aactgcactt gtattcccat cccatcatcc 720
tgggctttcg caagattcct atgggagtg gctcagtcg gtttctcctg gctcagttta 780
ctagtgccat ttgttcagt gttcgtagg ctttcccca ctgtttggct ttcagttata 840
tggatgatgt ggtattgggg gccaaagtctg tacaacatct tgagtcctt tttacctcta 900
ttaccaattt tcttttgtct ttgggtatac att 933

<210> 46
<211> 311
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 21-153 (Q129R/G145R) + EGF (serotype y) sequence

<400> 46

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
Page 23

sequence listing_ST25.txt

```

1           5           10           15
His Gln Leu Asp Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu
20
Ser His Asp Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu
35
Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu
50
Arg Cys Gln Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala
65
Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
85
Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
100
Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
115
Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
130
His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
145
Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
165
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
180
Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
195
Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
210
Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
225
Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
245

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sequence listing_ST25.txt

Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
260 265 270

Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
275 280 285

Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
290 295 300

Phe Cys Leu Trp Val Tyr Ile
305 310

<210> 47
<211> 792
<212> DNA
<213> artificial sequence

<220>
<223> 21-153 + STR-tag (streptavidin) (serotype y) sequence

<400> 47
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
ggcggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag 120
aacacaacat caggattcct aggaccctg ctcgtgttac aggcgggggtt tttcttggtg 180
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta 240
gggggagcac ccacgtgtcc tggccaaaat tcgcagtcac caacctccaa tcactcacca 300
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata 360
ttcctcttca tcctgctgct atgcctcatc ttcttggttg ttcttctgga ctaccaaggt 420
atgttgcccc tttgtcctct acttcagga acatcaacca ccagcacggg gccatgcaag 480
acctgcacga ttcctgctca aggaacctct atgtttccct cttggtgctg tacaaaacct 540
tcggacggaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta 600
tgggagtggg cctcagtcctg tttctcctgg ctcagtttac tagtgccatt tgttcagtgg 660
ttcgtagggc tttccccac tgtttggtt tcagttatat ggatgatgtg gtattggggg 720
ccaagtctgt acaacatctt gagtccttt ttacctctat taccaatttt cttttgtctt 780
tggtataca tt 792

<210> 48
<211> 264
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 21-153 + STR-tag (streptavidin)
(serotype y) sequence

sequence listing_ST25.txt

<400> 48

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Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1      5      10      15
His Gln Leu Asp Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala
20     25     30
Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly
35     40     45
Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu
50     55     60
Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu
65     70     75     80
Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser
85     90     95
Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp
100    105    110
Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys
115    120    125
Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val
130    135    140
Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys
145    150    155    160
Thr Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys
165    170    175
Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser
180    185    190
Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe
195    200    205
Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu
210    215    220
Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly
225    230    235    240
Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile

```

Phe Phe Cys Leu Trp Val Tyr Ile
260

<210> 49
<211> 792
<212> DNA
<213> artificial sequence

<220>
<223> 21-153 (Q129R) + STR (serotype y) sequence

<400> 49
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
ggcggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag 120
aacacaacat caggattcct aggacccttg ctctgtttac aggcgggggtt tttcttgttg 180
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggactttctt caattttcta 240
gggggagcac ccacgtgtcc tggccaaaat tcgcagtccc caacctcaa tcactcacca 300
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata 360
ttcctcttca tcctgctgct atgcctcatc ttcttggttg ttcttctgga ctaccaaggt 420
atgttgcccg tttgtcctct acttccagga acatcaacca ccagcacggg gccatgcaag 480
acctgcacga ttctgctcg aggaacctct atgtttccct cttgttgctg tacaaaacct 540
tcggacggaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta 600
tgggagtggg cctcagtcctg tttctcctgg ctcaagttac tagtgccatt tgttcagtgg 660
ttcgtagggc tttccccac tgtttggtt tcagttatat ggatgatgtg gtattggggg 720
ccaagtctgt acaacatctt gagtcccttt ttacctctat taccaatttt cttttgtctt 780
tggtataca tt 792

<210> 50
<211> 264
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 21-153 (Q129R) + STR (serotype y) sequence

<400> 50

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala
20 25 30

sequence listing_ST25.txt

Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly
35 40 45

Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu
50 55 60

Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu
65 70 75 80

Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser
85 90 95

Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp
100 105 110

Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys
115 120 125

Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val
130 135 140

Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys
145 150 155 160

Thr Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys
165 170 175

Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser
180 185 190

Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe
195 200 205

Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu
210 215 220

Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly
225 230 235 240

Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile
245 250 255

Phe Phe Cys Leu Trp Val Tyr Ile
260

<210> 51
<211> 792

sequence listing_ST25.txt

<212> DNA

<213> artificial sequence

<220>

<223> 21-153 (G145R) + STR (serotype y) sequence

<400> 51

```

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ggcggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag      120
aacacaacat caggattcct aggaccctg ctcgtgttac aggcgggggt tttcttggtg      180
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta      240
gggggagcac ccacgtgtcc tggccaaaat tcgcagtccc caacctcaa tcactcacca      300
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata      360
ttcctcttca tcctgctgct atgcctcatc ttcttggttg ttcttctgga ctaccaaggt      420
atgttgcccc tttgtcctct acttcagga acatcaacca ccagcacggg gccatgcaag      480
acctgcacga ttcctgctca aggaacctct atgtttcctt cttgttgctg tacaaaacct      540
tcggacagaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta      600
tgggagtggg cctcagtccg tttctcctgg ctcagtttac tagtgccatt tggtcagtgg      660
ttcgtagggc tttccccac tgtttggtt tcagttatat ggatgatgtg gtattggggg      720
ccaagtctgt acaacatctt gagtcccttt ttacctctat taccaatttt cttttgtctt      780
tgggtataca tt                                                    792

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<210> 52

<211> 264

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 21-153 (G145R) + STR (serotype y) sequence

<400> 52

```

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10          15

His Gln Leu Asp Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala
20          25          30

Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly
35          40          45

Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu
50          55          60

```

sequence listing_ST25.txt

Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu
65 70 75 80

Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser
85 90 95

Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp
100 105 110

Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Cys
115 120 125

Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val
130 135 140

Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys
145 150 155 160

Thr Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys
165 170 175

Cys Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser
180 185 190

Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe
195 200 205

Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu
210 215 220

Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly
225 230 235 240

Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile
245 250 255

Phe Phe Cys Leu Trp Val Tyr Ile
260

<210> 53

<211> 792

<212> DNA

<213> artificial sequence

<220>

<223> 21-153 (Q129R/G145R)/STR-tag (serotype y) sequence

<400> 53

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60

sequence listing_ST25.txt

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ggcgccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag 120
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acaagaatcc tcacaatacc acagagtcta gactcgtggt ggactttctt caattttcta 240
gggggagcac ccacgtgtcc tggccaaaat tcgcagtccc caacctcaa tcactcacca 300
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata 360
ttcctcttca tcctgctgct atgcctcatc ttcttggttg ttcttctgga ctaccaaggt 420
atgttgcccg tttgtcctct acttccagga acatcaacca ccagcacggg gccatgcaag 480
acctgcacga ttctgctcg aggaacctct atgtttccct cttgttgctg tacaaaacct 540
tcggacagaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta 600
tgggagtggg cctcagtccg tttctcctgg ctcatgttac tagtgccatt tgttcagtgg 660
ttcgtagggc tttccccac tgtttggtt tcagttatat ggatgatgtg gtattggggg 720
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tggtataca tt 792

```

<210> 54

<211> 264

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 21-153 (Q129R/G145R)/STR-tag (serotype y) sequence

<400> 54

```

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10           15

```

```

His Gln Leu Asp Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala
          20           25           30

```

```

Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly
          35           40           45

```

```

Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu
50           55           60

```

```

Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu
65           70           75           80

```

```

Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser
          85           90           95

```

```

Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp

```

sequence listing_ST25.txt

100

105

110

Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys
115 120 125

Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val
130 135 140

Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys
145 150 155 160

Thr Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys
165 170 175

Cys Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser
180 185 190

Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe
195 200 205

Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu
210 215 220

Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly
225 230 235 240

Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile
245 250 255

Phe Phe Cys Leu Trp Val Tyr Ile
260

<210> 55

<211> 1170

<212> DNA

<213> artificial sequence

<220>

<223> 33-153 + ZZ (serotype y) sequence

<400> 55

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cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcgcgca acacgatgaa 120

gccgtagaca acaaattcaa caaagaacaa caaaacgcgt tctatgagat cttacattta 180

cctaacttaa acgaagaaca acgaaacgcc ttcattccaaa gtttaaaaga tgaccaaacg 240

caaagcgcta accttttagc agaagctaaa aagctaaatg atgctcaggc gccgaaagta 300

gacaacaaat tcaacaaaga acaacaaaac gcgtttctatg agatcttaca tttacctaac 360

sequence listing_ST25.txt

```

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gctaaccttt tagcagaagc taaaaagcta aatgatgctc aggcgccgaa agcggccgcc   480
cctgcaccga acatggagaa cacaacatca ggattcctag gacccttgct cgtgttacag   540
gcgggggttt tcttgttgac aagaatcctc acaataccac agagtctaga ctcgtggtgg   600
acttctctca attttctagg gggagcacc acgtgtcctg gccaaaattc gcagtcccca   660
acctccaatc actcaccaac ctcttgctct ccaatttgct ctggctatcg ctggatgtgt   720
ctgcggcggt ttatcatatt cctcttcac ctgctgctat gcctcatctt cttgttggtt   780
cttctggact accaaggtat gttgcccggt tgtcctctac ttccaggaac atcaaccacc   840
agcacggggc catgcaagac ctgcacgatt cctgctcaag gaacctctat gtttccctct   900
tgttgctgta caaaccttc ggacggaaac tgcacttgta ttcccatccc atcatcctgg   960
gctttcgcaa gattcctatg ggagtgggcc tcagtccggt tctcctggct cagtttacta  1020
gtgccatttg ttcagtgggt cgtagggctt tccccactg tttggctttc agttatatgg  1080
atgatgtggt attggggggc aagtctgtac aacatcttga gtcccttttt acctctatta  1140
ccaattttct tttgtctttg ggtatacatt  1170

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<210> 56

<211> 390

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 33-153 + ZZ (serotype y) sequence

<400> 56

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys
35 40 45

Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn
50 55 60

Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
65 70 75 80

Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln
85 90 95

sequence_listing_ST25.txt

Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
100 105 110

Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala
115 120 125

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
130 135 140

Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala
145 150 155 160

Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
165 170 175

Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
180 185 190

Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
195 200 205

Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
210 215 220

Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
225 230 235 240

Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
245 250 255

Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
260 265 270

Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
275 280 285

Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
290 295 300

Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
305 310 315 320

Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
325 330 335

Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
340 345 350

sequence_listing_ST25.txt

Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
355 360 365

Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
370 375 380

Cys Leu Trp Val Tyr Ile
385 390

<210> 57
<211> 1170
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (Q129R) + ZZ (serotype y) sequence

<400> 57
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cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcgcgca acacgatgaa 120
gccgtagaca acaaattcaa caaagaacaa caaaacgcgt tctatgagat cttacattta 180
cctaacttaa acgaagaaca acgaaacgcc ttcattccaaa gtttaaaaga tgacccaagc 240
caaagcgcta accttttagc agaagctaaa aagctaaatg atgctcaggc gccgaaagta 300
gacaacaaat tcaacaaaga acaacaaaac gcgttctatg agatcttaca ttacctaac 360
ttaaacgaag aacaacgaaa cgccttcatt caaagtttaa aagatgaccc aagccaaagc 420
gctaaccttt tagcagaagc taaaaagcta aatgatgctc aggcgccgaa agcggccgcc 480
cctgcaccga acatggagaa cacaacatca ggattcctag gacccttgct cgtgttacag 540
gcgggggtttt tcttgttgac aagaatcctc acaataccac agagtctaga ctcgtggtgg 600
acttctctca attttctagg gggagcacc acgtgtcctg gccaaaattc gcagtcccca 660
acctccaatc actcaccaac ctcttgtcct ccaatttgtc ctggctatcg ctggatgtgt 720
ctgcggcggtt ttatcatatt cctcttcatt ctgctgctat gcctcatctt cttgttggtt 780
cttctggact accaaggtat gttgcccgtt tgtcctctac ttccaggaac atcaaccacc 840
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tgttgctgta caaaccttc ggacggaaac tgcacttgta ttcccatccc atcatcctgg 960
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gtgccatttg ttcagtgggt cgtagggtt tccccactg tttggctttc agttatatgg 1080
atgatgtggt attggggggc aagtctgtac aacatcttga gtcccttttt acctctatta 1140
ccaattttct tttgtctttg ggtatacatt 1170

sequence listing_ST25.txt

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<210> 58
<211> 390
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 33-153 (Q129R) + ZZ (serotype y)
sequence

<400> 58
Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1          5          10          15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
          20          25          30

Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys
          35          40          45

Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn
50          55          60

Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
65          70          75          80

Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln
          85          90          95

Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
100         105         110

Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala
115         120         125

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
130         135         140

Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala
145         150         155         160

Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
165         170         175

Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
180         185         190

Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
195         200         205

```

sequence listing_ST25.txt

Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
210 215 220

Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
225 230 235 240

Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
245 250 255

Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
260 265 270

Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
275 280 285

Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
290 295 300

Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
305 310 315 320

Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
325 330 335

Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
340 345 350

Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
355 360 365

Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
370 375 380

Cys Leu Trp Val Tyr Ile
385 390

<210> 59
<211> 1170
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (G145R) + ZZ (serotype y) sequence

<400> 59
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gccgtagaca acaaattcaa caaagaacaa caaaacgcgt tctatgagat cttacattta 180
Page 37

sequence listing_ST25.txt

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cctaacttaa acgaagaaca acgaaacgcc ttcattccaaa gtttaaaaga tgacccaagc 240
caaagcgcta accttttagc agaagctaaa aagctaaatg atgctcaggc gccgaaagta 300
gacaacaaat tcaacaaaga acaacaaaac gcgttctatg agatcttaca ttacctaac 360
ttaaacgaag aacaacgaaa cgccttcac caaagtttaa aagatgaccc aagccaaagc 420
gctaaccttt tagcagaagc taaaaagcta aatgatgctc aggcgccgaa agcggccgcc 480
cctgcaccga acatggagaa cacaacatca ggattcctag gacccctgct cgtgttacag 540
gcgggggttt tcttggtgac aagaatcctc acaataccac agagtctaga ctcgtggtgg 600
acttctctca attttctagg gggagcacc cagtgctctg gccaaaattc gcagtcccca 660
acctccaatc actcaccaac ctcttgctct ccaatttgct ctggctatcg ctggatgtgt 720
ctgcggcggt ttatcatatt cctcttcac ctgctgctat gcctcatctt cttgttggtt 780
cttctggact accaaggtat gttgcccggt tgcctcttac ttccaggaac atcaaccacc 840
agcacggggc catgcaagac ctgcacgatt cctgctcaag gaacctctat gtttccctct 900
tgttgctgta caaaccttc ggacagaaac tgcacttgta ttcccatccc atcatcctgg 960
gctttcgcaa gattcctatg ggagtgggcc tcagtccggt tctcctggct cagtttacta 1020
gtgccatttg ttcagtgggt cgtagggctt tccccactg tttggctttc agttatatgg 1080
atgatgtggt attggggggc aagtctgtac aacatcttga gtcccttttt acctctatta 1140
ccaattttct tttgtctttg ggtatacatt 1170

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<210> 60
<211> 390
<212> PRT
<213> artificial sequence

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<220>
<223> Proteins corresponding to 33-153 (G145R) + ZZ (serotype y)
sequence

```

```

<400> 60

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Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10          15

```

```

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20          25          30

```

```

Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys
35          40          45

```

```

Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn
50          55          60

```

sequence listing_ST25.txt

Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
 65 70 75 80
 Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln
 85 90 95
 Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
 100 105 110
 Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala
 115 120 125
 Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
 130 135 140
 Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala
 145 150 155 160
 Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
 165 170 175
 Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
 180 185 190
 Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
 195 200 205
 Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
 210 215 220
 Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
 225 230 235 240
 Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
 245 250 255
 Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
 260 265 270
 Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
 275 280 285
 Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
 290 295 300
 Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
 305 310 315 320

sequence listing_ST25.txt

Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
325 330 335

Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
340 345 350

Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
355 360 365

Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
370 375 380

Cys Leu Trp Val Tyr Ile
385 390

<210> 61
<211> 1170
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (Q129R/G145R) + ZZ (serotype y) sequence

<400> 61
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cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcgcgca acacgatgaa 120
gccgtagaca acaaattcaa caaagaacaa caaaacgcgt tctatgagat cttacattta 180
cctaacttaa acgaagaaca acgaaacgcc ttcattccaa gtttaaaaga tgacccaagc 240
caaagcgcta accttttagc agaagctaaa aagctaaatg atgctcaggc gccgaaagta 300
gacaacaaat tcaacaaaga acaacaaaac gcgttctatg agatcttaca ttacctaac 360
ttaaacgaag aacaacgaaa cgccttcatt caaagtttaa aagatgaccc aagccaaagc 420
gctaaccttt tagcagaagc taaaaagcta aatgatgctc aggcgccgaa agcggccgcc 480
cctgcaccga acatggagaa cacaacatca ggattcctag gacccctgct cgtgttacag 540
gcgggggttt tcttgttgac aagaatcctc acaataccac agagtctaga ctcgtggtgg 600
acttctctca attttctagg gggagcacc acgtgtcctg gccaaaattc gcagtcccca 660
acctccaatc actcaccaac ctcttgctct ccaatttgct ctggctatcg ctggatgtgt 720
ctgcggcggt ttatcatatt cctcttcatt ctgctgctat gcctcatctt cttgttggtt 780
cttctggact accaaggtat gttgcccggt tgtcctctac ttccaggaac atcaaccacc 840
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tgttgctgta caaaccttc ggacagaaac tgcacttgta ttcccatccc atcatcctgg 960
gctttcgcaa gattcctatg ggagtgggcc tcagtccggt tctcctggct cagtttacta 1020

sequence listing_ST25.txt

gtgccatttg ttcagtgggt cgtagggcct tccccactg tttggctttc agttatatgg 1080
atgatgtggt attgggggcc aagtctgtac aacatcttga gtcccttttt acctctatta 1140
ccaattttct tttgtctttg ggtatacatt 1170

<210> 62
<211> 390
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 33-153 (Q129R/G145R) + ZZ (serotype y)
sequence

<400> 62

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys
35 40 45

Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn
50 55 60

Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
65 70 75 80

Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln
85 90 95

Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
100 105 110

Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala
115 120 125

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
130 135 140

Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala
145 150 155 160

Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
165 170 175

sequence_listing_ST25.txt

Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
180 185 190

Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
195 200 205

Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
210 215 220

Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
225 230 235 240

Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
245 250 255

Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
260 265 270

Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
275 280 285

Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
290 295 300

Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
305 310 315 320

Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
325 330 335

Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
340 345 350

Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
355 360 365

Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
370 375 380

Cys Leu Trp Val Tyr Ile
385 390

<210> 63
<211> 969
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 + EGF (serotype y) sequence

sequence listing_ST25.txt

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<400> 63
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gaatgcccgc tgtctcatga cggttactgc ctgcatgatg gcgtatgcat gtacatcgaa      180
gctctggaca aatacgcgat caactgtggt gtaggttaca tcggcgaacg ttgccagtat      240
cgcgacctga aatggtggga actgcgtaag gcggccgccc ctgcaccgaa catggagaac      300
acaacatcag gattcctagg acccctgctc gtgttacagg cggggttttt cttgttgaca      360
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tcttgtcctc caatttgtcc tggctatcgc tggatgtgtc tgcggcgttt tatcatattc      540
ctcttcatcc tgctgctatg cctcatcttc ttgttggttc ttctggacta ccaaggtagt      600
ttgcccgttt gtcctctact tccaggaaca tcaaccacca gcacggggcc atgcaagacc      660
tgcacgattc ctgctcaagg aacctctatg tttccctctt gttgctgtac aaaaccttcg      720
gacggaaact gcacttgat tcccatccca tcactctggg ctttcgcaag attcctatgg      780
gagtgggcct cagtccgttt ctcctggctc agtttactag tgccatttgt tcagtgggtc      840
gtagggtttt cccccactgt ttggctttca gttatatgga tgatgtggta ttgggggcca      900
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gtatacatt                                         969

```

```

<210> 64
<211> 323
<212> PRT
<213> artificial sequence

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```

<220>
<223> Proteins corresponding to 33-153 + EGF (serotype y). sequence

```

```

<400> 64

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Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10          15

```

```

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20          25          30

```

```

Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly
35          40          45

```

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Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys
50          55          60

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sequence listing_ST25.txt

Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr
 65 70 75 80
 Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro
 85 90 95
 Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
 100 105 110
 Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
 115 120 125
 Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
 130 135 140
 Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
 145 150 155 160
 Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
 165 170 175
 Phe Ile Ile Phe Leu Phe Ile Leu Leu Cys Leu Ile Phe Leu Leu
 180 185 190
 Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
 195 200 205
 Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
 210 215 220
 Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
 225 230 235 240
 Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
 245 250 255
 Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
 260 265 270
 Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
 275 280 285
 Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
 290 295 300
 Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
 305 310 315 320

sequence listing_ST25.txt

Val Tyr Ile

<210> 65
 <211> 969
 <212> DNA
 <213> artificial sequence

<220>
 <223> 33-153 (Q129R) + EGF (serotype y) sequence

<400> 65
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 cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcatgaa ctctgattcc 120
 gaatgcccgc tgtctcatga cggttactgc ctgcatgatg gcgcatgcat gtacatcgaa 180
 gctctggaca aatacgcatg caactgtgtt gtaggttaca tcggcgaacg ttgccagtat 240
 cgcgacctga aatggtggga actgcgtaag gcggccgccc ctgcaccgaa catggagaac 300
 acaacatcag gattcctagg acccctgctc gtgttacagg cggggttttt cttgttgaca 360
 agaatcctca caataccaca gagtctagac tcgtggtgga cttctctcaa ttttctaggg 420
 ggagcaccca cgtgtcctgg ccaaaattcg cagtcccca cctccaatca ctcaccaacc 480
 tcttgtcctc caatttgtcc tggctatcgc tggatgtgtc tgcggcgttt tatcatattc 540
 ctcttcatcc tgctgctatg cctcatcttc ttgttggttc ttctggacta ccaaggtagt 600
 ttgcccgttt gtcctctact tccaggaaca tcaaccacca gcacggggcc atgcaagacc 660
 tgcacgattc ctgctcgagg aacctctatg tttccctctt gttgctgtac aaaaccttcg 720
 gacggaaact gcacttgat tcccatccca tcatcctggg ctttcgcaag attcctatgg 780
 gagtgggcct cagtccgttt ctcttggtc agtttactag tgccatttgt tcagtgggtc 840
 gtagggcttt cccccactgt ttggctttca gttatatgga tgatgtggta ttgggggcca 900
 agtctgtaca acatcttgag tcccttttta cctctattac caattttctt ttgtctttgg 960
 gtatacatt 969

<210> 66
 <211> 323
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 33-153 (Q129R) + EGF (serotype y) sequence

<400> 66

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

sequence listing_ST25.txt

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly
35 40 45

Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys
50 55 60

Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr
65 70 75 80

Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro
85 90 95

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
100 105 110

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
115 120 125

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
130 135 140

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
145 150 155 160

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
165 170 175

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
180 185 190

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
195 200 205

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
210 215 220

Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
225 230 235 240

Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
245 250 255

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
260 265 270

sequence listing_ST25.txt

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
275 280 285

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
290 295 300

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
305 310 315 320

Val Tyr Ile

<210> 67
<211> 969
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (G145R) + EGF (serotype y) sequence

<400> 67
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cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcatgaa ctctgattcc 120
gaatgcccgc tgtctcatga cggttactgc ctgcatgatg gcgatgcat gtacatcgaa 180
gctctggaca aatacgcgat caactgtgtt gtaggttaca tcggcgaacg ttgccagtat 240
cgcgacctga aatggtggga actgcgtaag gcggccgccc ctgcaccgaa catggagaac 300
acaacatcag gattcctagg acccctgctc gtgttacagg cggggttttt cttgttgaca 360
agaatcctca caataccaca gagtctagac tcgtggtgga cttctctcaa ttttctaggg 420
ggagcaccca cgtgtcctgg ccaaaattcg cagtcccaa cctccaatca ctcaccaacc 480
tcttgtcctc caatttgtcc tggctatcgc tggatgtgtc tgcggcgttt tatcatattc 540
ctcttcatcc tgctgctatg cctcatcttc ttgttggttc ttctggacta ccaaggtatg 600
ttgcccgttt gtccttact tccaggaaca tcaaccacca gcacggggcc atgcaagacc 660
tgcacgattc ctgctcaagg aacctctatg tttccctctt gttgctgtac aaaaccttcg 720
gacagaaact gcacttgat tcccatcca tcacctggg ctttcgcaag attcctatgg 780
gagtgggcct cagtccgttt ctctggctc agtttactag tgccatttgt tcagtggttc 840
gtagggcttt cccccactgt ttggctttca gttatatgga tgatgtggta ttgggggcca 900
agtctgtaca acatcttgag tcccttttta cctctattac caattttctt ttgtctttgg 960
gtatacatt 969

<210> 68

sequence listing_ST25.txt

<211> 323

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 33-153 (G145R) + EGF (serotype y)
sequence

<400> 68

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly
35 40 45

Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys
50 55 60

Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr
65 70 75 80

Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro
85 90 95

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
100 105 110

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
115 120 125

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
130 135 140

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
145 150 155 160

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
165 170 175

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
180 185 190

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
195 200 205

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
Page 48

sequence listing_ST25.txt

210

215

220

Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
225 230 235 240

Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
245 250 255

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
260 265 270

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
275 280 285

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
290 295 300

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
305 310 315 320

Val Tyr Ile

<210> 69

<211> 969

<212> DNA

<213> artificial sequence

<220>

<223> 33-153 (Q129R/G145R) + EGF (serotype y) sequence

<400> 69

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cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcatgaa ctctgattcc	120
gaatgcccgc tgtctcatga cggttactgc ctgcatgatg gcgtatgcat gtacatcgaa	180
gctctggaca aatacgcgat caactgtggt gtaggttaca tcggcgaacg ttgccagtat	240
cgcgacctga aatggtggga actgcgtaag gcggccgccc ctgcaccgaa catggagAAC	300
acaacatcag gattcctagg acccctgctc gtgttacagg cggggttttt cttgttgaca	360
agaatcctca caataccaca gagtctagac tcgtggtgga cttctctcaa ttttctaggg	420
ggagcaccga cgtgtcctgg ccaaaattcg cagtcccca cctccaatca ctcaccaacc	480
tcttgtcctc caatttgctc tggctatcgc tggatgtgtc tgcggcgttt tatcatattc	540
ctcttcatcc tgctgctatg cctcatcttc ttgttggttc ttctggacta ccaaggatatg	600
ttgcccgttt gtcctctact tccaggaaca tcaaccacca gcacggggcc atgcaagacc	660
tgcacgattc ctgctcgagg aacctctatg tttccctctt gttgctgtac aaaaccttcg	720

sequence listing_ST25.txt

gacagaaact gcacttgat tcccatccca tcatacctggg ctttcgcaag attcctatgg 780
gagtgggcct cagtcggtt ctctgggctc agtttactag tgccatttgt tcagtgggtc 840
gtagggcttt cccccactgt ttggctttca gttatatgga tgatgtggta ttgggggcca 900
agtctgtaca acatcttgag tcccttttta cctctattac caattttctt ttgtctttgg 960
gtatacatt 969

<210> 70
<211> 323
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 33-153 (Q129R/G145R) + EGF (serotype y) sequence

<400> 70

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly
35 40 45

Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys
50 55 60

Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr
65 70 75 80

Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro
85 90 95

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
100 105 110

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
115 120 125

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
130 135 140

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
145 150 155 160

sequence listing_ST25.txt

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
165 170 175

Phe Ile Ile Phe Leu Phe Ile Leu Leu Cys Leu Ile Phe Leu Leu
180 185 190

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
195 200 205

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
210 215 220

Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
225 230 235 240

Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
245 250 255

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
260 265 270

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
275 280 285

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
290 295 300

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
305 310 315 320

Val Tyr Ile

<210> 71
<211> 828
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 + STR-tag (serotype y) sequence

<400> 71
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgctggag ccacccgcag 120
ttcgaaaaag cggccgcccc tgcaccgaac atggagaaca caacatcagg attcctagga 180
cccctgctcg tgttacaggc ggggtttttc ttgttgacaa gaatcctcac aataccacag 240
agtctagact cgtggtggac ttctctcaat tttctagggg gagcaccac gtgtcctggc 300

sequence listing_ST25.txt

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caaaattcgc agtccccaac ctccaatcac tcaccaacct cttgtcctcc aatttgcct 360
ggctatcgct ggatgtgtct gcggcgtttt atcatattcc tcttcacct gctgctatgc 420
ctcatcttct tgttggttct tctggactac caaggatatgt tgcccgtttg tcctctactt 480
ccaggaacat caaccaccag cacggggcca tgcaagacct gcacgattcc tgctcaagga 540
acctctatgt ttccctcttg ttgctgtaca aaaccttcgg acggaaactg cacttgattt 600
cccatcccat catcctgggc ttctgcaaga ttctatggg agtgggcctc agtccgtttc 660
tcctggctca gtttactagt gccatttggt cagtggttcg tagggctttc cccactggt 720
tggctttcag ttatatggat gatgtggtat tgggggcca gtctgtacaa catcttgagt 780
ccctttttac ctctattacc aattttcttt tgtctttggg tatacatt 828

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<210> 72

<211> 276

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 33-153 + STR-tag (serotype y) sequence

<400> 72

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala
35 40 45

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
50 55 60

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
65 70 75 80

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
85 90 95

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
100 105 110

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
115 120 125

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
130 135 140

sequence listing_ST25.txt

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
145 150 155 160

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
165 170 175

Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
180 185 190

Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
195 200 205

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
210 215 220

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
225 230 235 240

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
245 250 255

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
260 265 270

Trp Val Tyr Ile
275

<210> 73
<211> 828
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (Q129R) + STR-tag (serotype y) sequence

<400> 73
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cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgctggag ccacccgcag 120
ttcgaaaaag cggccgcccc tgcaccgaac atggagaaca caacatcagg attcctagga 180
cccctgctcg tgttacaggc ggggtttttc ttgttgacaa gaatcctcac aataccacag 240
agtctagact cgtggtggac ttctctcaat ttctagggg gagcaccac gtgtcctggc 300
caaaattcgc agtccccaac ctccaatcac tcaccaacct cttgtcctcc aatttgcct 360
ggctatcgct ggatgtgtct gcggcgtttt atcatattcc tcttcattct gctgctatgc 420
ctcatcttct tgttggttct tctggactac caaggatatgt tgcccgtttg tcctctactt 480

sequence listing_ST25.txt

ccaggaacat caaccaccag cacggggcca tgcaagacct gcacgattcc tgctcgagga 540
acctctatgt ttccctcttg ttgctgtaca aaaccttcgg acggaaactg cacttgatt 600
cccatcccat catcctgggc tttcgcaaga ttcctatggg agtgggcctc agtccgtttc 660
tcctggctca gtttactagt gccatttggt cagtggttcg tagggctttc cccactgtt 720
tggctttcag ttatatggat gatgtggtat tggggggcaa gtctgtacaa catcttgagt 780
ccctttttac ctctattacc aattttcttt tgtctttggg tatacatt 828

<210> 74

<211> 276

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 33-153 (Q129R) + STR-tag (serotype y)
sequence

<400> 74

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala
35 40 45

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
50 55 60

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
65 70 75 80

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
85 90 95

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
100 105 110

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
115 120 125

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
130 135 140

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
145 150 155 160

sequence listing_ST25.txt

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
165 170 175

Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
180 185 190

Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
195 200 205

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
210 215 220

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
225 230 235 240

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
245 250 255

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
260 265 270

Trp Val Tyr Ile
275

<210> 75
<211> 828
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (G145R) + STR-tag (serotype y) sequence

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ttcgaaaaag cggccgcccc tgcaccgaac atggagaaca caacatcagg attcctagga 180
cccctgctcg tgttacaggc ggggtttttc ttgttgacaa gaatcctcac aataccacag 240
agtctagact cgtggtggac ttctctcaat ttcttagggg gagcaccac gtgtcctggc 300
caaaattcgc agtccccaac ctccaatcac tcaccaacct cttgtcctcc aatttgcct 360
ggctatcgct ggatgtgtct gcggcgtttt atcatattcc tcttcacct gctgctatgc 420
ctcatcttct tgttggttct tctggactac caaggatatgt tgcccgtttg tcctctactt 480
ccaggaacat caaccaccag cacggggcca tgcaagacct gcacgattcc tgctcaagga 540
acctctatgt ttccctcttg ttgctgtaca aaaccttcgg acagaaactg cacttgatt 600
cccatcccat catcctgggc tttcgcaaga ttccataggg agtgggcctc agtccgtttc 660

sequence listing_ST25.txt

tcctggctca gtttactagt gccatttggt cagtgggtcg tagggctttc cccactggt 720
 tggctttcag ttatatggat gatgtggtat tgggggcca gtctgtacaa catcttgagt 780
 ccctttttac ctctattacc aattttcttt tgtctttggg tatacatt 828

<210> 76

<211> 276

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 33-153 (G145R) + STR-tag (serotype y)
 sequence

<400> 76

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
 20 25 30

Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala
 35 40 45

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
 50 55 60

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
 65 70 75 80

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
 85 90 95

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
 100 105 110

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
 115 120 125

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
 130 135 140

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
 145 150 155 160

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
 165 170 175

sequence listing_ST25.txt

Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
180 185 190

Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
195 200 205

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
210 215 220

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
225 230 235 240

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
245 250 255

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
260 265 270

Trp Val Tyr Ile
275

<210> 77
<211> 828
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (Q129R/G145R) + STR-tag (serotype y) sequence

<400> 77
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cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgctggag ccacccgcag 120
ttcgaaaaag cggccgcccc tgcaccgaac atggagaaca caacatcagg attcctagga 180
cccctgctcg tgttacaggc ggggtttttc ttgttgacaa gaatcctcac aataccacag 240
agtctagact cgtggtggac ttctctcaat ttcttagggg gagcaccac gtgtcctggc 300
caaaattcgc agtccccaac ctccaatcac tcaccaacct cttgtcctcc aatttgcct 360
ggctatcgct ggatgtgtct gcggcgtttt atcatattcc tcttcatcct gctgctatgc 420
ctcatcttct tgttggttct tctggactac caaggtatgt tgcccgtttg tcctctactt 480
ccaggaacat caaccaccag cacggggcca tgcaagacct gcacgattcc tgctcgagga 540
acctctatgt ttccctcttg ttgctgtaca aaaccttcgg acagaaactg cacttgatt 600
cccatcccat catcctgggc ttctgcaaga ttctatggg agtgggcctc agtccgtttc 660
tcctggctca gtttactagt gccatttggt cagtggttcg tagggctttc cccactggt 720
tggctttcag ttatatggat gatgtggtat tgggggcca gtctgtacaa catcttgagt 780

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<210> 78

<211> 276

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 33-153 (Q129R/G145R) + STR-tag (serotype y) sequence

<400> 78

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala
35 40 45

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
50 55 60

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
65 70 75 80

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
85 90 95

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
100 105 110

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
115 120 125

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
130 135 140

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
145 150 155 160

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
165 170 175

Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
180 185 190

Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
Page 58

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
210 215 220

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
225 230 235 240

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
245 250 255

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
260 265 270

Trp Val Tyr Ile
275

<210> 79
<211> 1221
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 + ZZ (serotype y) sequence

<400> 79
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tgccagagg caaatcaggt aggagcgggc ggccgcgcgc aacacgatga agccgtagac 180
aacaattca acaagaaca acaaacgcg ttctatgaga tttacattt acctaactta 240
aacgaagaac aacgaaacgc cttcatccaa agtttaaaag atgaccaag ccaaagcgct 300
aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagt agacaacaaa 360
ttcaacaaag aacaacaaa cgcgttctat gagatcttac atttacctaa cttaaacgaa 420
gaacaacgaa acgccttcat ccaaagttaa aaagatgacc caagccaaag cgtaacctt 480
ttagcagaag ctaaaaagct aaatgatgct caggcgccga aagcggccgc ccctgcaccg 540
aacatggaga acacaacatc aggattccta ggacccttgc tcgtgttaca ggcgggggtt 600
ttcttggtga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc 660
aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcccc aacctccaat 720
cactcaccaa cctcttgtcc tccaatttgt cctggctatc gctggatgtg tctgcggcgt 780
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taccaaggta tgttgcccgt ttgtcctcta cttccaggaa catcaaccac cagcacgggg 900
ccatgcaaga cctgcacgat tcctgtctca ggaacctcta tgtttccctc ttgttgctgt 960

sequence listing_ST25.txt

acaaaacctt cggacggaaa ctgcacttgt attcccatcc catcatcctg ggctttcgca 1020
 agattcctat gggagtgggc ctgagtcctg ttctcctggc tcagtttact agtgccattt 1080
 gttcagtggg tcgtagggct ttccccact gtttggtttt cagttatatg gatgatgtgg 1140
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 ttttgccttt gggatacat t 1221

<210> 80
 <211> 407
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 50-153 + ZZ (serotype y) sequence
 <400> 80

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
 20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
 35 40 45

Ala Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn
 50 55 60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
 65 70 75 80

Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro
 85 90 95

Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
 100 105 110

Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
 115 120 125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
 130 135 140

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
 145 150 155 160

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala
 Page 60

sequence_listing_ST25.txt

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165                                     170                                     175
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180
Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
195                200                205
Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
210                215                220
Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
225                230                235
His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
245                250                255
Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
260                265                270
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
275                280                285
Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
290                295                300
Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
305                310                315                320
Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
325                330                335
Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
340                345                350
Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
355                360                365
Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
370                375                380
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
385                390                395                400
Phe Cys Leu Trp Val Tyr Ile
405

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sequence listing_ST25.txt

<210> 81
 <211> 1221
 <212> DNA
 <213> artificial sequence

<220>
 <223> 50-153 (Q129R) + ZZ (serotype y) sequence

<400> 81
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 aacaaattca acaaaagaaca acaaaaacgcg ttctatgaga tcttacattt acctaactta 240
 aacgaagaac aacgaaacgc cttcatccaa agtttaaaag atgacccaag ccaaagcgct 300
 aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagt agacaacaaa 360
 ttcaacaaag aacaacaaaa cgcgttctat gagatcttac atttacctaa cttaaacgaa 420
 gaacaacgaa acgccttcat ccaaagttta aaagatgacc caagccaaag cgctaacctt 480
 ttagcagaag ctaaaaagct aaatgatgct caggcgccga aagcggccgc ccctgcaccg 540
 aacatggaga acacaacatc aggattccta ggacccttgc tcgtgttaca ggcgggggtt 600
 ttcttggtga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc 660
 aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcccc aacctccaat 720
 cactcaccaa cctcttgtcc tccaatttgt cctggctatc gctggatgtg tctgcggcgt 780
 tttatcatat tcctcttcat cctgctgcta tgcctcatct tcttggtggt tcttctggac 840
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 ccatgcaaga cctgcacgat tcctgctcga ggaacctcta tgtttccctc ttgttgctgt 960
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 gttcagtggc tcgtagggct ttccccact gtttggtgtt cagttatatg gatgatgtgg 1140
 tattgggggc caagtctgta caacatcttg agtccctttt tacctctatt accaattttc 1200
 ttttgtcttt gggatacat t 1221

<210> 82
 <211> 407
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 50-153 (Q129R) + ZZ (serotype y) sequence

<400> 82

sequence listing_ST25.txt

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Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1      5      10      15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
      20      25      30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
      35      40      45

Ala Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn
      50      55      60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
      65      70      75      80

Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro
      85      90      95

Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
      100      105      110

Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
      115      120      125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
      130      135      140

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
      145      150      155      160

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala
      165      170      175

Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
      180      185      190

Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
      195      200      205

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
      210      215      220

Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
      225      230      235      240

His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
      245      250      255

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sequence_listing_ST25.txt

Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
260 265 270

Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
275 280 285

Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
290 295 300

Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
305 310 315 320

Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
325 330 335

Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
340 345 350

Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
355 360 365

Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
370 375 380

Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
385 390 395 400

Phe Cys Leu Trp Val Tyr Ile
405

<210> 83
<211> 1221
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 (G145R) + ZZ (serotype y) sequence

<400> 83
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tgGCCagagg caaatcaggt aggagcgggc ggccgcgcgc aacacgatga agccgtagac 180
aacaattca acaaagaaca aaaaaacgCG ttctatgaga ttttacattt acctaactta 240
aacgaagaac aacgaaacgc cttcatccaa agtttaaaag atgaccaag ccaaagcgct 300
aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagt agacaacaaa 360
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sequence_listing_ST25.txt

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ttcttggtga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc 660
aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcctc aacctccaat 720
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taccaaggta tggtgcccgt ttgtcctcta cttccaggaa catcaaccac cagcacgggg 900
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ttttgtcttt gggatacat t 1221

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<210> 84

<211> 407

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 50-153 (G145R) + ZZ (serotype y)
sequence

<400> 84

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
35 40 45

Ala Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn
50 55 60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65 70 75 80

Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro
85 90 95

sequence listing_ST25.txt

Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
100 105 110

Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
115 120 125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
130 135 140

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
145 150 155 160

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala
165 170 175

Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
180 185 190

Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
195 200 205

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
210 215 220

Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
225 230 235 240

His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
245 250 255

Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
260 265 270

Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
275 280 285

Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
290 295 300

Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
305 310 315 320

Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
325 330 335

Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser

sequence listing_ST25.txt
345 350

340

Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
355 360 365

Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
370 375 380

Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
385 390 395 400

Phe Cys Leu Trp Val Tyr Ile
405

<210> 85
<211> 1221
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 (Q129R/G145R) + ZZ (serotype y) sequence

<400> 85
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aaaaacctt cggacagaaa ctgcacttgt attcccatcc catcatcctg ggctttcgca 1020
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sequence_listing_ST25.txt

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ttttgtcttt gggatacat t 1221

<210> 86
<211> 407
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 50-153 (Q129R/G145R) + ZZ (serotype y)
sequence

<400> 86

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
35 40 45

Ala Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn
50 55 60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65 70 75 80

Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro
85 90 95

Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
100 105 110

Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
115 120 125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
130 135 140

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
145 150 155 160

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala
165 170 175

sequence listing_ST25.txt

Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
180 185 190

Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
195 200 205

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
210 215 220

Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
225 230 235 240

His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
245 250 255

Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
260 265 270

Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
275 280 285

Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
290 295 300

Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
305 310 315 320

Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
325 330 335

Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
340 345 350

Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
355 360 365

Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
370 375 380

Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
385 390 395 400

Phe Cys Leu Trp Val Tyr Ile
405

<210> 87
<211> 1020
<212> DNA

sequence listing_ST25.txt

<213> artificial sequence

<220>

<223> 50-153 + EGF (serotype y) sequence

<400> 87

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tcagtccgtt tctcctggct cagtttacta gtgccatttg ttcagtgggt cgtagggcct      900
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<210> 88

<211> 340

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 50-153 + EGF (serotype y) sequence

<400> 88

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Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10           15

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His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20           25           30

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Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
35           40           45

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sequence_listing_ST25.txt

Ala Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp
50 55 60

Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp
65 70 75 80

Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln
85 90 95

Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala
100 105 110

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
115 120 125

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
130 135 140

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
145 150 155 160

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
165 170 175

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
180 185 190

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
195 200 205

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
210 215 220

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
225 230 235 240

Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
245 250 255

Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
260 265 270

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
275 280 285

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
290 295 300

sequence listing_ST25.txt

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
305 310 315 320

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
325 330 335

Trp Val Tyr Ile
340

<210> 89
<211> 1020
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 (Q129R) + EGF (serotype y) sequence

<400> 89
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tgccagagg caaatcaggt aggagcgggc ggccgcatga actctgattc cgaatgcccg 180
ctgtctcatg acggttactg cctgcatgat ggcgtatgca tgtacatcga agctctggac 240
aaatacgcat gcaactgtgt tgtaggttac atcggcgaac gttgccagta tcgcgacctg 300
aaatggtggg aactgcgtaa ggcggccgcc cctgcaccga acatggagaa cacaacatca 360
ggattcctag gaccctgct cgtgttacag gcggggtttt tcttgttgac aagaatcctc 420
acaataccac agagtctaga ctctgtgtgg acttctctca attttctagg gggagcacc 480
acgtgtcctg gccaaaattc gcagtcccca acctccaatc actcaccaac ctcttgtcct 540
ccaatttgtc ctggctatcg ctggatgtgt ctgcggcggt ttatcatatt cctcttcac 600
ctgctgctat gcctcatctt cttgttggtt cttctggact accaaggat gttgcccgtt 660
tgtcctctac ttccaggaa atcaaccacc agcacggggc catgcaagac ctgcacgatt 720
cctgctcgag gaacctctat gtttccctct tgttgctgta caaaccttc ggacggaaac 780
tgcacttgta ttcccatccc atcatcctgg gctttcgcaa gattcctatg ggagtgggcc 840
tcagtccgtt tctcctggct cagtttacta gtgccatttg ttcagtgggt cgtagggctt 900
tccccactg tttggctttc agttatatgg atgatgtggt attgggggcc aagtctgtac 960
aacatcttga gtcccttttt acctctatta ccaattttct tttgtctttg ggtatacatt 1020

<210> 90
<211> 340
<212> PRT
<213> artificial sequence

<220>

sequence listing_ST25.txt

<223> Proteins corresponding to 50-153 (Q129R) + EGF (serotype y)
sequence

<400> 90

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
35 40 45

Ala Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp
50 55 60

Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp
65 70 75 80

Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln
85 90 95

Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala
100 105 110

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
115 120 125

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
130 135 140

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
145 150 155 160

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
165 170 175

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
180 185 190

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
195 200 205

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
210 215 220

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
225 230 235 240

sequence_listing_ST25.txt

Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
245 250 255

Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
260 265 270

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
275 280 285

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
290 295 300

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
305 310 315 320

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
325 330 335

Trp Val Tyr Ile
340

<210> 91
<211> 1020
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 (G145R) + EGF (serotype y) sequence

<400> 91
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cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
tggccagagg caaatcaggt aggagcgggc ggccgcatga actctgattc cgaatgcccg 180
ctgtctcatg acggttactg cctgcatgat ggcgtatgca tgtacatcga agctctggac 240
aaatacgcat gcaactgtgt tgtaggttac atcggcgaac gttgccagta tcgcgacctg 300
aaatgggtggg aactgcgtaa ggcgggccgcc cctgcaccga acatggagaa cacaacatca 360
ggattcctag gaccctgct cgtgttacag gcggggtttt tcttgttgac aagaatcctc 420
acaataccac agagtctaga ctctgtgtgg acttctctca attttctagg gggagcacc 480
acgtgtcctg gccaaaattc gcagtccca acctccaatc actcaccaac ctcttgctct 540
ccaatttgtc ctggctatcg ctggatgtgt ctgcggcggt ttatcatatt cctcttcac 600
ctgctgctat gcctcatctt cttgttggtt cttctggact accaaggtat gttgcccgtt 660
tgtcctctac ttccaggaac atcaaccacc agcacggggc catgcaagac ctgcacgatt 720

sequence_listing_ST25.txt

cctgctcaag gaacctctat gtttcctct tgttgctgta caaaccttc ggacagaaac 780
 tgcacttgta ttcccatccc atcatcctgg gctttcgcaa gattcctatg ggagtgggcc 840
 tcagtccgtt tctcctggct cagtttacta gtgccatttg ttcagtgggt cgtagggcct 900
 tccccactg tttggctttc agttatatgg atgatgtggt attgggggcc aagtctgtac 960
 aacatcttga gtcccttttt acctctatta ccaattttct tttgtctttg ggtatacatt 1020

<210> 92

<211> 340

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 50-153 (G145R) + EGF (serotype y)
 sequence

<400> 92

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
 20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
 35 40 45

Ala Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp
 50 55 60

Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp
 65 70 75 80

Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln
 85 90 95

Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala
 100 105 110

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
 115 120 125

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
 130 135 140

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
 145 150 155 160

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro

sequence listing_ST25.txt

165

170

175

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
180 185 190

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
195 200 205

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
210 215 220

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
225 230 235 240

Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
245 250 255

Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
260 265 270

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
275 280 285

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
290 295 300

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
305 310 315 320

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
325 330 335

Trp Val Tyr Ile
340

<210> 93
<211> 1020
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 (Q129R/G145R) + EGF (serotype y) sequence

<400> 93
atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
tgccagagg caaatcaggt aggagcgggc ggccgcatga actctgattc cgaatgcccg 180
ctgtctcatg acggttactg cctgcatgat ggcgtatgca tgtacatcga agctctggac 240

sequence listing_ST25.txt

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aaatacgcac gcaactgtgt tgtaggttac atcggcgaac gttgccagta tcgcgacctg 300
aaatgggtggg aactgcgtaa ggcgccgcc cctgcaccga acatggagaa cacaacatca 360
ggattcctag gacccctgct cgtgttacag gcggggtttt tcttggtgac aagaatcctc 420
acaataccac agagtctaga ctctgtgttg acttctctca attttctagg gggagcacc 480
acgtgtcctg gccaaaattc gcagtcacca acctccaatc actcaccaac ctcttgctct 540
ccaatttgtc ctggctatcg ctggatgtgt ctgcggcggt ttatcatatt cctcttcac 600
ctgtctctat gcctcatctt cttgttggtt cttctggact accaaggat gttgcccgtt 660
tgtcctctac ttccaggaac atcaaccacc agcacggggc catgcaagac ctgcacgatt 720
cctgctcgag gaacctctat gtttccctct tgttgctgta caaaccttc ggacagaaac 780
tgcacttgta ttcccatccc atcatcctgg gctttcgcaa gattcctatg ggagtgggcc 840
tcagtccgtt tctcctggct cagtttacta gtgccatttg ttcagtgggt cgtagggtt 900
tccccactg tttggctttc agttatatgg atgatgtggt attgggggcc aagtctgtac 960
aacatcttga gtcccttttt acctctatta ccaattttct tttgtctttg ggtatacatt 1020

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<210> 94

<211> 340

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 50-153 (Q129R/G145R) + EGF (serotype y)
sequence

<400> 94

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Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10           15

```

```

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20           25           30

```

```

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
35           40           45

```

```

Ala Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp
50           55           60

```

```

Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp
65           70           75           80

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Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln
85           90           95

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sequence listing_ST25.txt

Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala
100 105 110

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
115 120 125

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
130 135 140

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
145 150 155 160

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
165 170 175

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
180 185 190

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
195 200 205

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
210 215 220

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
225 230 235 240

Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
245 250 255

Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
260 265 270

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
275 280 285

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
290 295 300

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
305 310 315 320

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
325 330 335

Trp Val Tyr Ile
340

sequence listing_ST25.txt

<210> 95
<211> 879
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 + STR-tag (serotype y) sequence

<400> 95
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cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
tggccagagg caaatcaggt aggagcgggc ggccgctgga gccacccgca gttcgaaaaa 180
gcggccgccc ctgcaccgaa catggagaac acaacatcag gattcctagg acccctgctc 240
gtgttacagg cgggggtttt cttgttgaca agaatcctca caataccaca gagtctagac 300
tcgtggtgga cttctctcaa ttttctaggg ggagcaccca cgtgtcctgg ccaaaattcg 360
cagtcccaa cctccaatca ctcaccaacc tcttgcctc caatttgtcc tggctatcgc 420
tggatgtgtc tgcggcggtt tatcatattc ctcttcaccc tgctgctatg cctcatcttc 480
ttgttggttc ttctggacta ccaaggatat ttgcccgttt gtcctctact tccaggaaca 540
tcaaccacca gcacggggcc atgcaagacc tgcacgattc ctgctcaagg aacctctatg 600
tttccctctt gttgctgtac aaaaccttcg gacggaaact gcacttgat tcccatccca 660
tcctcctggg ctttcgcaag attcctatgg gagtgggcct cagtccgttt ctcctggctc 720
agtttactag tgccatttgt tcagtgggtc gtagggcttt cccccactgt ttggctttca 780
gttatatgga tgatgtggtt ttgggggcca agtctgtaca acatcttgag tcccttttta 840
cctctattac caattttctt ttgtcttttg gtatacatt 879

<210> 96
<211> 293
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 50-153 + STR-tag (serotype y) sequence

<400> 96

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
35 40 45

sequence listing_ST25.txt

Ala Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro
50 55 60

Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
65 70 75 80

Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
85 90 95

Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
100 105 110

Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
115 120 125

Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
130 135 140

Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
145 150 155 160

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
165 170 175

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
180 185 190

Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
195 200 205

Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
210 215 220

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
225 230 235 240

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
245 250 255

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
260 265 270

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
275 280 285

Leu Trp Val Tyr Ile
290

sequence listing_ST25.txt

<210> 97
 <211> 879
 <212> DNA
 <213> artificial sequence

<220>
 <223> 50-153 (Q129R) + STR-tag (serotype y) sequence

<400> 97
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 cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
 tggccagagg caaatcaggt aggagcgggc ggccgctgga gccaccgcga gttcgaaaaa 180
 gcggccgccc ctgcaccgaa catggagaac acaacatcag gattcctagg acccctgctc 240
 gtgttacagg cgggggtttt cttgttgaca agaatcctca caataccaca gagtctagac 300
 tcgtggtgga cttctctcaa ttttctaggg ggagcaccca cgtgtcctgg ccaaaattcg 360
 cagtcccaa cctccaatca ctcaccaacc tcttgtcctc caatttgtcc tggctatcgc 420
 tggatgtgtc tgcggcgttt tatcatattc ctcttcatcc tgctgctatg cctcatcttc 480
 ttgttggttc ttctggacta ccaaggtatg ttgcccgttt gtcctctact tccaggaaca 540
 tcaaccacca gcacggggcc atgcaagacc tgcacgattc ctgctcgagg aacctctatg 600
 tttccctctt gttgctgtac aaaaccttcg gacggaaact gcacttgat tcccatccca 660
 tcatcctggg ctttcgcaag attcctatgg gagtgggcct cagtccgttt ctcctggctc 720
 agtttactag tgccatttgt tcagtggttc gtagggcctt cccccactgt ttggctttca 780
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 cctctattac caattttctt ttgtctttgg gtatacatt 879

<210> 98
 <211> 293
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 50-153 (Q129R) + STR-tag (serotype y) sequence

<400> 98

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
 20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
 35 40 45

sequence listing_ST25.txt

Ala Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro
50 55 60

Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
65 70 75 80

Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
85 90 95

Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
100 105 110

Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
115 120 125

Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
130 135 140

Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
145 150 155 160

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
165 170 175

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
180 185 190

Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
195 200 205

Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
210 215 220

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
225 230 235 240

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
245 250 255

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
260 265 270

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
275 280 285

Leu Trp Val Tyr Ile
290

sequence listing_ST25.txt

<210> 99
 <211> 879
 <212> DNA
 <213> artificial sequence

<220>
 <223> 50-153 (G145R) + STR-tag (serotype y) sequence

<400> 99
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 cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
 tggccagagg caaatcaggt aggagcgggc ggccgctgga gccaccgcga gttcgaaaaa 180
 gcggccgccc ctgcaccgaa catggagaac acaacatcag gattcctagg acccctgctc 240
 gtgttacagg cggggttttt cttgttgaca agaatcctca caataccaca gagtctagac 300
 tcgtggtgga cttctctcaa ttttctaggg ggagcaccca cgtgtcctgg ccaaatttcg 360
 cagtcccca cctccaatca ctaccaacc tcttgcctc caatttgtcc tggctatcgc 420
 tggatgtgtc tgcggcggtt tatcatattc ctcttcatcc tgctgctatg cctcatcttc 480
 ttgttggttc ttctggacta ccaaggtatg ttgcccggtt gtcctctact tccaggaaca 540
 tcaaccacca gcacggggcc atgcaagacc tgcacgattc ctgctcaagg aacctctatg 600
 tttccctctt gttgctgtac aaaaccttcg gacagaaact gcacttgtat tcccatccca 660
 tcctcctggg ctttcgcaag attcctatgg gagtgggcct cagtccgttt ctcttggtc 720
 agtttactag tgccatttgt tcagtgggtc gtagggcttt cccccactgt ttggctttca 780
 gttatatgga tgatgtggta ttgggggccca agtctgtaca acatcttgag tcccttttta 840
 cctctattac caattttctt ttgtctttgg gtatacatt 879

<210> 100
 <211> 293
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 50-153 (G145R) + STR-tag (serotype y) sequence

<400> 100

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
 20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
 35 40 45

sequence listing_ST25.txt

Ala Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro
50 55 60

Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
65 70 75 80

Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
85 90 95

Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
100 105 110

Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
115 120 125

Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
130 135 140

Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
145 150 155 160

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
165 170 175

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
180 185 190

Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
195 200 205

Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
210 215 220

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
225 230 235 240

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
245 250 255

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
260 265 270

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
275 280 285

Leu Trp Val Tyr Ile

sequence listing_ST25.txt

290

<210> 101
<211> 879
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 (Q129R/G145R) + STR-tag (serotype y) sequence

<400> 101
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cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
tggccagagg caaatcaggt aggagcgggc ggccgctgga gccaccgcga gttcgaaaaa 180
gcggccgccc ctgcaccgaa catggagaac acaacatcag gattcctagg acccctgctc 240
gtgttacagg cgggggtttt cttgttgaca agaatcctca caataccaca gagtctagac 300
tcgtggtgga cttctctcaa ttttctaggg ggagcaccca cgtgtcctgg ccaaaattcg 360
cagtcccaa cctccaatca ctaccaacc tcttgtctc caatttgctc tggctatcgc 420
tggatgtgtc tgcggcggtt tatcatattc ctcttcattc tgctgctatg cctcatcttc 480
ttgttggttc ttctggacta ccaaggatg ttgcccgttt gtcctctact tccaggaaca 540
tcaaccacca gcacggggcc atgcaagacc tgcacgattc ctgctcgagg aacctctatg 600
tttccctctt gttgctgtac aaaaccttcg gacagaaact gcacttgat tcccatccca 660
tcacctggg ctttcgcaag attcctatgg gagtgggcct cagtccgttt ctctggctc 720
agtttactag tgccatttgt tcagtggttc gtagggcttt cccccactgt ttggctttca 780
gttatatgga tgatgtggtt ttgggggcca agtctgtaca acatcttgag tcccttttta 840
cctctattac caattttctt ttgtctttgg gtatacatt 879

<210> 102
<211> 293
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 50-153 (Q129R/G145R) + STR-tag
(serotype y) sequence

<400> 102
Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15
His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
Page 85

Ala Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro
50 55 60

Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
65 70 75 80

Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
85 90 95

Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
100 105 110

Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
115 120 125

Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
130 135 140

Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
145 150 155 160

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
165 170 175

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
180 185 190

Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
195 200 205

Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
210 215 220

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
225 230 235 240

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
245 250 255

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
260 265 270

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
275 280 285

sequence listing_ST25.txt

Leu Trp Val Tyr Ile
290

<210> 103
<211> 1167
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 + ZZ (serotype d; claim12) sequence

<400> 103
atgggagggtt ggtcttccaa acctcggaaa ggcattggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gacggcggcc gcgcgcaaca cgatgaagcc 120
gtagacaaca aattcaacaa agaacaacaa aacgcgttct atgagatctt acatttacct 180
aacttaaacg aagaacaacg aaacgccttc atccaaagtt taaaagatga cccaagccaa 240
agcgctaacc ttttagcaga agctaaaaag cttaatgatg ctgaggcgcc gaaagtagac 300
aacaattca acaaagaaca acaaacgcg ttctatgaga tcttacattt acctaactta 360
aacgaagaac aacgaaacgc cttcatccaa agtttaaaag atgacccaag ccaaagcgct 420
aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagc ggccgcccct 480
gcaccgaaca tggagaacac aacatcagga ttcctaggac ccctgctcgt gttacaggcg 540
gggtttttct tgttgacaag aatcctcaca ataccacaga gtctagactc gtggtggact 600
tctctcaatt ttctaggggg agcaccacg tgtcctggcc aaaattcgca gtccccaacc 660
tccaatcact caccaacctc ttgtcctcca atttgtcctg gctatcgctg gatgtgtctg 720
cggcgtttta tcatattcct cttcatcctg ctgctatgcc tcatcttctt gttggttctt 780
ctggactacc aaggatatgtt gcccgtttgt cctctacttc caggaaacatc aaccaccagc 840
acggggccat gcaagacctg cacgattcct gctcaaggaa cctctatgtt tccctcttgt 900
tgctgtacaa aaccttcgga cggaactgc acttgatttc ccatcccatc atcctgggct 960
ttcgaagat tcctatggga gtgggcctca gtccgtttct cctggctcag ttactagtg 1020
ccatttgttc agtggttcgt agggctttcc cccactgttt ggctttcagt tatatggatg 1080
atgtggtatt gggggccaag tctgtacaac atcttgagtc cttttttacc tctattacca 1140
atcttctttt gtctttgggt atacatt 1167

<210> 104
<211> 389
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 32-164 + ZZ (serotype d; claim12)
sequence

sequence listing_ST25.txt

<400> 104

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Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1      5      10      15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
      20      25      30

Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu
      35      40      45

Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu
      50      55      60

Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln
65      70      75      80

Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala
      85      90      95

Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr
      100      105      110

Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe
      115      120      125

Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala
      130      135      140

Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro
145      150      155      160

Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
      165      170      175

Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
      180      185      190

Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
      195      200      205

Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
      210      215      220

Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
225      230      235      240

Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe

```


sequence_listing_ST25.txt

245

250

255

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
260 265 270

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
275 280 285

Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
290 295 300

Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
305 310 315 320

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
325 330 335

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
340 345 350

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
355 360 365

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
370 375 380

Leu Trp Val Tyr Ile
385

<210> 105
<211> 1167
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 (Q129R) + ZZ (serotype d) sequence

<400> 105
atgggaggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gacggcggcc gcgcgcaaca cgatgaagcc 120
gtagacaaca aattcaacaa agaacaacaa aacgcgttct atgagatctt acatttacct 180
aacttaaacg aagaacaacg aaacgccttc atccaaagtt taaaagatga cccaagccaa 240
agcgctaacc ttttagcaga agctaaaaag cttaatgatg ctcaggcgcc gaaagtagac 300
aacaattca acaaagaaca acaaaacgcg ttctatgaga tcttacattt acctaactta 360
aacgaagaac aacgaaacgc cttcatccaa agtttaaaag atgacccaag ccaaagcgct 420
aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagc ggccgcccct 480

sequence listing_ST25.txt

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gcaccgaaca tggagaacac aacatcagga ttcctaggac ccctgctcgt gttacaggcg 540
gggtttttct tgttgacaag aatcctcaca ataccacaga gtctagactc gtggtggact 600
tctctcaatt ttctaggggg agcaccacag tgtcctggcc aaaattcgca gtccccaacc 660
tccaatcact caccaacctc ttgtcctcca atttgtcctg gctatcgctg gatgtgtctg 720
cggcgtttta tcatattcct cttcatcctg ctgctatgcc tcatcttctt gttggttctt 780
ctggactacc aaggatatgtt gcccgtttgt cctctacttc caggaacatc aaccaccagc 840
acggggccat gcaagacctg cacgattcct gctcgaggaa cctctatggt tccctcttgt 900
tgctgtacaa aaccttcgga cggaaactgc acttgatttc ccatcccatc atcctgggct 960
ttcgcaagat tcctatggga gtgggcctca gtccgtttct cctggctcag ttactagtg 1020
ccatttgttc agtggttcgt agggctttcc cccactgttt ggctttcagt tatatggatg 1080
atgtggtatt gggggccaag tctgtacaac atcttgagtc cttttttacc tctattacca 1140
attttctttt gtctttgggt atacatt 1167
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<210> 106
 <211> 388
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 32-164 (Q129R) + ZZ (serotype d) sequence

<400> 106

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
 20 25 30

Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu
 35 40 45

Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu
 50 55 60

Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln
 65 70 75 80

Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala
 85 90 95

Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr
 100 105 110

sequence listing_ST25.txt

Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe
 115 120 125
 Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala
 130 135 140
 Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro
 145 150 155 160
 Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
 165 170 175
 Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
 180 185 190
 Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
 195 200 205
 Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
 210 215 220
 Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
 225 230 235 240
 Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
 245 250 255
 Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
 260 265 270
 Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
 275 280 285
 Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
 290 295 300
 Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
 305 310 315 320
 Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
 325 330 335
 Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
 340 345 350
 Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu

355

sequence listing_ST25.txt
360 365

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
370 375 380

Leu Trp Val Tyr
385

<210> 107
<211> 1167
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 (G145R) + ZZ (serotype d) sequence

<400> 107
atgggagggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
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gtagacaaca aattcaacaa agaacaacaa aacgcgttct atgagatctt acatttacct 180
aacttaaacg aagaacaacg aaacgccttc atccaaagtt taaaagatga cccaagccaa 240
agcgctaacc ttttagcaga agctaaaaag ctaaattgatg ctcaggcgcc gaaagtagac 300
aaciaattca acaaagaaca acaaaacgcg ttctatgaga tcttacattt acctaactta 360
aacgaagaac aacgaaacgc cttcatccaa agtttaaaag atgacccaag ccaaagcgct 420
aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagc ggccgcccct 480
gcaccgaaca tggagaacac aacatcagga ttcttaggac ccctgctcgt gttacaggcg 540
gggtttttct tgttgacaag aatcctcaca ataccacaga gtctagactc gtggtggact 600
tctctcaatt ttctaggggg agcaccacag tgtcctggcc aaaattcgca gtccccaacc 660
tccaatcact caccaacctc ttgtcctcca atttgtcctg gctatcgctg gatgtgtctg 720
cggcgtttta tcatattcct cttcatcctg ctgctatgcc tcatcttctt gttggttctt 780
ctggactacc aaggatatgtt gcccgtttgt cctctacttc caggaacatc aaccaccagc 840
acggggccat gcaagacctg cacgattcct gctcaaggaa cctctatggt tccctcttgt 900
tgctgtacaa aaccttcgga cagaaactgc acttgatttc ccatcccatc atcctgggct 960
ttcgcaagat tcctatggga gtgggcctca gtccgtttct cctggctcag ttacttagtg 1020
ccatttgttc agtggttcgt agggctttcc cccactgttt ggctttcagt tatatggatg 1080
atgtggtatt gggggccaag tctgtacaac atcttgagtc cttttttacc tctattacca 1140
atcttctttt gtctttgggt atacatt 1167

<210> 108
<211> 389

sequence listing_ST25.txt

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 32-164 (G145R) + ZZ (serotype d)
sequence

<400> 108

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
20 25 30

Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu
35 40 45

Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu
50 55 60

Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln
65 70 75 80

Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala
85 90 95

Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr
100 105 110

Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe
115 120 125

Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala
130 135 140

Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro
145 150 155 160

Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
165 170 175

Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
180 185 190

Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
195 200 205

Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
210 215 220

sequence listing_ST25.txt

Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
 225 230 235 240

Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
 245 250 255

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
 260 265 270

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
 275 280 285

Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
 290 295 300

Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
 305 310 315 320

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
 325 330 335

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
 340 345 350

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
 355 360 365

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
 370 375 380

Leu Trp Val Tyr Ile
 385

<210> 109
 <211> 1167
 <212> DNA
 <213> artificial sequence

<220>
 <223> 32-164 (Q129R/G145R) + ZZ-tag (serotype d) sequence

<400> 109
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 cctctgggat tctttcccga tcaccagttg gacggcggcc gcgcgcaaca cgatgaagcc 120
 gtagacaaca aattcaaca agaacaaca aacgcgttct atgagatctt acatttacct 180
 aacttaaacg aagaacaacg aaacgccttc atccaaagtt taaaagatga cccaagccaa 240

sequence listing_ST25.txt

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agcgctaacc ttttagcaga agctaaaaag ctaaagatg ctcaggcgcc gaaagtagac 300
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aacgaagaac aacgaaacgc cttcatccaa agttttaaag atgacccaag ccaaagcgct 420
aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagc ggccgcccct 480
gcaccgaaca tggagaacac aacatcagga ttcctaggac ccctgctcgt gttacaggcg 540
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tccaatcact caccaacctc ttgtcctcca atttgtcctg gctatcgctg gatgtgtctg 720
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acggggccat gcaagacctg cagcattcct gctcgaggaa cctctatggt tccctcttgt 900
tgctgtacaa aaccttcgga cagaaactgc acttgatttc ccatcccatc atcctgggct 960
ttcgcaagat tcctatggga gtgggcctca gtccgtttct cctggctcag ttactagtg 1020
ccatttggtc agtggttcgt agggctttcc cccactgttt ggctttcagt tatatggatg 1080
atgtggtatt gggggccaag tctgtacaac atcttgagtc cttttttacc tctattacca 1140
attttctttt gtctttgggt atacatt 1167

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<210> 110

<211> 389

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 32-164 (Q129R/G145R) + ZZ-tag (serotype d) sequence

<400> 110

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Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1           5           10           15

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Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
          20           25           30

```

```

Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu
          35           40           45

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Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu
          50           55           60

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Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln
65           70           75           80

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sequence listing_ST25.txt

Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala
85 90 95

Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr
100 105 110

Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe
115 120 125

Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala
130 135 140

Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro
145 150 155 160

Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
165 170 175

Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
180 185 190

Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
195 200 205

Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
210 215 220

Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
225 230 235 240

Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
245 250 255

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
260 265 270

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
275 280 285

Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
290 295 300

Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
305 310 315 320

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
325 330 335

sequence listing_ST25.txt

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
340 345 350

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
355 360 365

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
370 375 380

Leu Trp Val Tyr Ile
385

<210> 111
<211> 966
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 + EGF (serotype d) sequence

<400> 111
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tgcccgtgt ctcattgacgg ttactgcctg catgatggcg tatgcatgta catcgaagct 180
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gacctgaaat ggtgggaact gcgtaaggcg gccgcccctg caccgaacat ggagaacaca 300
acatcaggat tcctaggacc cctgctcgtg ttacaggcgg gggtttttctt gttgacaaga 360
atcctcacia taccacagag tctagactcg tgggtggactt ctctcaattt tctaggggga 420
gcaccacgt gtcctggcca aaattcgcag tccccaacct ccaatcactc accaacctct 480
tgtcctccaa ttgtcctggt ctatcgtgtg atgtgtctgc ggcgttttat catattcctc 540
ttcatcctgc tgctatgcct catcttcttg ttggttcttc tggactacca aggtatgttg 600
cccgtttgtc ctctacttcc aggaacatca accaccagca cggggccatg caagacctgc 660
acgattcctg ctcaagggaac ctctatgttt ccctcttggt gctgtacaaa accttcggac 720
ggaaactgca cttgtattcc catcccatca tcctgggctt tcgcaagatt cctatgggag 780
tgggcctcag tccgtttctc ctggctcagt ttactagtgc catttggtca gtggttcgta 840
gggctttccc cactgtttg gctttcagtt atatggatga tgtggtattg ggggccaagt 900
ctgtacaaca tcttgagtcc ctttttacct ctattaccaa ttttcttttg tctttgggta 960
tacatt 966

<210> 112

sequence listing_ST25.txt

<211> 322

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 32-164 + EGF (serotype d) sequence

<400> 112

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
20 25 30

Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr
35 40 45

Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr
50 55 60

Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg
65 70 75 80

Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn
85 90 95

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
100 105 110

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
115 120 125

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
130 135 140

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
145 150 155 160

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
165 170 175

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
180 185 190

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
195 200 205

Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
210 215 220

sequence listing_ST25.txt

Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
225 230 235 240

Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
245 250 255

Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
260 265 270

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
275 280 285

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
290 295 300

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
305 310 315 320

Tyr Ile

<210> 113
<211> 966
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 (Q129R) + EGF (serotype d) sequence

<400> 113
atgggaggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gacggcggcc gcatgaactc tgattccgaa 120
tgcccgtgt ctcattgacg ttactgcctg catgatggcg tatgcatgta catcgaagct 180
ctggacaaat acgcatgcaa ctgtgttgta ggttacatcg gcgaacgttg ccagtatcgc 240
gacctgaaat ggtgggaact gcgtaaggcg gccgcccctg caccgaacat ggagaacaca 300
acatcaggat tcctaggacc cctgctcgtg ttacaggcgg ggtttttctt gttgacaaga 360
atcctcacia taccacagag tctagactcg tgggtggactt ctctcaattt tctaggggga 420
gcaccacgt gtcctggcca aaattcgcag tccccaacct ccaatcactc accaacctct 480
tgtcctccaa ttgtcctg ctatcgctgg atgtgtctgc ggcgttttat catattcctc 540
ttcatcctgc tgctatgcct catcttcttg ttggttcttc tggactacca aggtatgttg 600
cccgtttgtc ctctacttcc aggaacatca accaccagca cggggccatg caagacctgc 660
acgattcctg ctcgaggaac ctctatgttt ccctcttggt gctgtacaaa accttcggac 720

sequence listing_ST25.txt

ggaaactgca cttgtattcc catcccatca tcctgggctt tcgcaagatt cctatgggag 780
 tgggcctcag tccgtttctc ctggctcagt ttactagtgc catttggtca gtggttcgta 840
 gggctttccc ccactgtttg gctttcagtt atatggatga tgtgggtattg ggggccaaagt 900
 ctgtacaaca tcttgagtcc ctttttacct ctattaccaa ttttcttttg tctttgggta 960
 tacatt 966

<210> 114
 <211> 322
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 32-164 (Q129R) + EGF (serotype d)
 sequence

<400> 114

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
 20 25 30

Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr
 35 40 45

Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr
 50 55 60

Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg
 65 70 75 80

Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn
 85 90 95

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
 100 105 110

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
 115 120 125

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
 130 135 140

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
 145 150 155 160

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
 Page 100

sequence listing_ST25.txt

```

165                               170                               175
Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
180                               185                               190
Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
195                               200                               205
Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
210                               215                               220
Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
225                               230                               235
Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
245                               250                               255
Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
260                               265                               270
Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
275                               280                               285
Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
290                               295                               300
Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
305                               310                               315                               320

```

Tyr Ile

```

<210> 115
<211> 966
<212> DNA
<213> artificial sequence

```

```

<220>
<223> 32-164 (G145R) + EGF (serotype d) sequence

```

```

<400> 115
atgggaggtt ggtcttccaa acctcgga aa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gacggcggcc gcatgaactc tgattccgaa 120
tgcccgtgt ctcattgacgg ttactgcctg catgatggcg tatgcatgta catcgaagct 180
ctggacaaat acgcatgcaa ctgtgttgta ggttacatcg gcgaacgttg ccagtatcgc 240
gacctgaaat ggtgggaact gcgtaaggcg gccgcccctg caccgaacat ggagaacaca 300
acatcaggat tcctaggacc cctgctcgtg ttacaggcgg ggtttttctt gttgacaaga 360

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sequence listing_ST25.txt

```

atcctcacia taccacagag tctagactcg tgggtggactt ctctcaattt tctaggggga 420
gcacccacgt gtcctggcca aaattcgag tccccaacct ccaatcactc accaacctct 480
tgtcctcaa tttgtcctgg ctatcgctgg atgtgtctgc ggcgttttat catattcctc 540
ttcatcctgc tgctatgcct catcttcttg ttggttcttc tggactacca aggtatgttg 600
cccgtttgtc ctctacttcc aggaacatca accaccagca cggggccatg caagacctgc 660
acgattcctg ctcaaggaac ctctatgttt cctctttggt gctgtacaaa accttcggac 720
agaaactgca cttgtattcc catcccatca tcctgggctt tcgcaagatt cctatgggag 780
tgggcctcag tccgtttctc ctggctcagt ttactagtgc catttggtca gtggttcgta 840
gggctttccc ccactgtttg gctttcagtt atatggatga tgtggtattg ggggccaagt 900
ctgtacaaca tcttgagtcc ctttttacct ctattaccaa ttttcttttg tctttgggta 960
tacatt 966

```

<210> 116
 <211> 322
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 32-164 (G145R) + EGF (serotype d) sequence

<400> 116

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
 20 25 30

Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr
 35 40 45

Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr
 50 55 60

Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg
 65 70 75 80

Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn
 85 90 95

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
 100 105 110

sequence listing_ST25.txt

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
115 120 125

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
130 135 140

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
145 150 155 160

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
165 170 175

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
180 185 190

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
195 200 205

Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
210 215 220

Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
225 230 235 240

Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
245 250 255

Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
260 265 270

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
275 280 285

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
290 295 300

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
305 310 315 320

Tyr Ile

<210> 117
<211> 966
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 (Q129R/G145R) + EGF (serotype d) sequence
Page 103

sequence listing_ST25.txt

```

<400> 117
atggggagggtt ggtcttccaa acctcggaaa ggcattggga cgaatctttc tgttcccaat    60
cctctgggat tctttcccga tcaccagttg gacggcggcc gcatgaactc tgattccgaa    120
tgcccgtgt ctcattgacgg ttactgcctg catgatggcg tatgcatgta catcgaagct    180
ctggacaaat acgcatgcaa ctgtgttgta gggtacatcg gcgaacgttg ccagtatcgc    240
gacctgaaat ggtgggaact gcgtaaggcg gccgcccctg caccgaacat ggagaacaca    300
acatcaggat tcctaggacc cctgctcgtg ttacaggcgg gggttttctt gttgacaaga    360
atcctcacia taccacagag tctagactcg tgggtggactt ctctcaattt tctaggggga    420
gcaccacagt gtcctggcca aaattcgag tccccaacct ccaatcactc accaacctct    480
tgtcctcaa tttgtcctgg ctatcgtgg atgtgtctgc ggcgttttat catattctc    540
ttcatcctgc tgctatgcct catcttcttg ttggttcttc tggactacca aggtatgttg    600
cccgtttgtc ctctacttcc aggaacatca accaccagca cggggccatg caagacctgc    660
acgattcctg ctcgaggaa cctctatgtt cctcttctgt gctgtacaaa accttcggac    720
agaaactgca cttgtattcc catcccatca tcctgggctt tcgcaagatt cctatgggag    780
tgggcctcag tccgtttctc ctggctcagt ttactagtgc catttgttca gtggttcgta    840
gggctttccc ccactgtttg gctttcagtt atatggatga tgtggtattg ggggccaagt    900
ctgtacaaca tcttgagtcc ctttttacct ctattaccaa ttttcttttg tctttgggta    960
tacatt                                           966

```

```

<210> 118
<211> 322
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 32-164 (Q129R/G145R) + EGF (serotype d)
sequence

```

```

<400> 118
Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1          5          10          15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
          20          25          30

Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr
          35          40          45

Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr
          50          55          60

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sequence listing_ST25.txt

Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg
65 70 75 80

Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn
85 90 95

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
100 105 110

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
115 120 125

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
130 135 140

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
145 150 155 160

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
165 170 175

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
180 185 190

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
195 200 205

Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
210 215 220

Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
225 230 235 240

Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
245 250 255

Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
260 265 270

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
275 280 285

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
290 295 300

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
305 310 315 320

sequence listing_ST25.txt

Tyr Ile

<210> 119
<211> 825
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 + STR-tag (streptavidin) (serotype d) sequence

<400> 119
atgggaggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gacggcggcc gctggagcca cccgcagttc 120
gaaaaagcgg cgcgccctgc accgaacatg gagaacacaa catcaggatt cctaggaccc 180
ctgctcgtgt tacaggcggg gtttttcttg ttgacaagaa tcctcacaat accacagagt 240
ctagactcgt ggtggacttc tctcaatttt ctagggggag caccacgtg tcctggccaa 300
aattcgcagt ccccaacctc caatcactca ccaacctctt gtcctccaat ttgtcctggc 360
tatcgctgga tgtgtctgcg gcgttttatc atattcctct tcattcctgt gctatgcctc 420
atcttcttgt tggttcttct ggactaccaa ggtatgttgc ccgtttgtcc tctacttcca 480
ggaacatcaa ccaccagcac ggggccatgc aagacctgca cgattcctgc tcaaggaacc 540
tctatgtttc cctcttggtg ctgtacaaaa ccttcggacg gaaactgcac ttgtattccc 600
atcccatcat cctgggcttt cgcaagattc ctatgggagt gggcctcagt ccgtttctcc 660
tggctcagtt tactagtgcc atttgttcag tggttcgtag ggctttcccc cactgtttgg 720
ctttcagtta tatggatgat gtggtattgg gggccaagtc tgtacaacat cttgagtccc 780
ttttacctc tattaccaat tttcttttgt ctttgggtat acatt 825

<210> 120
<211> 275
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 32-164 + STR-tag (streptavidin)
(serotype d) sequence

<400> 120

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
20 25 30

sequence listing_ST25.txt

Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro
35 40 45

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
50 55 60

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
65 70 75 80

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
85 90 95

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
100 105 110

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
115 120 125

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
130 135 140

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
145 150 155 160

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
165 170 175

Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
180 185 190

Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
195 200 205

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
210 215 220

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
225 230 235 240

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
245 250 255

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
260 265 270

Val Tyr Ile
275

sequence listing_ST25.txt

<210> 121
<211> 825
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 (Q129R) + STR (serotype d) sequence

<400> 121
atgggaggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gacggcggcc gctggagcca cccgcagttc 120
gaaaaagcgg ccgcccctgc accgaacatg gagaacacaa catcaggatt cctaggaccc 180
ctgctcgtgt tacaggcggg gtttttcttg ttgacaagaa tcctcacaat accacagagt 240
ctagactcgt ggtggacttc tctcaatttt ctagggggag caccacagtg tcctggccaa 300
aattcgcagt ccccaacctc caatcactca ccaacctctt gtcttccaat ttgtcctggc 360
tatcgctgga tgtgtctgcg gcgttttatc atattcctct tcattcctgct gctatgcctc 420
atcttcttgt tggttcttct ggactaccaa ggtatgttgc ccgtttgtcc tctacttcca 480
ggaacatcaa ccaccagcac ggggccatgc aagacctgca cgattcctgc tcgaggaacc 540
tctatgtttc cctcttggtg ctgtacaaaa ccttcggacg gaaactgcac ttgtattccc 600
atcccatcat cctgggcttt cgcaagattc ctatgggagt gggcctcagt ccgtttctcc 660
tggctcagtt tactagtgcc atttgttcag tggttcgtag ggctttcccc cactgtttgg 720
ctttcagtta tatggatgat gtggtattgg gggccaagtc tgtacaacat cttgagtccc 780
ttttacctc tattaccaat tttcttttgt ctttgggtat acatt 825

<210> 122
<211> 275
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 32-164 (Q129R) + STR (serotype d) sequence

<400> 122

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
20 25 30

Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro
35 40 45

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
Page 108

sequence listing_ST25.txt

50

55

60

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
65 70 75 80

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
85 90 95

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
100 105 110

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
115 120 125

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
130 135 140

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
145 150 155 160

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
165 170 175

Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
180 185 190

Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
195 200 205

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
210 215 220

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
225 230 235 240

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
245 250 255

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
260 265 270

Val Tyr Ile
275

<210> 123

<211> 825

<212> DNA

<213> artificial sequence

sequence listing_ST25.txt

<220>

<223> 32-164 (G145R) + STR (serotype d) sequence

<400> 123

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atgggaggtt ggtcttccaa acctcgaaa ggcatgggga cgaatctttc tgttcccaat    60
cctctgggat tctttcccga tcaccagttg gacggcggcc gctggagcca cccgcagttc    120
gaaaaagcgg ccgcccctgc accgaacatg gagaacacaa catcaggatt cctaggaccc    180
ctgctcgtgt tacaggcggg gtttttcttg ttgacaagaa tcctcacaat accacagagt    240
ctagactcgt ggtggacttc tctcaatttt ctagggggag caccacgtg tcctggccaa    300
aattcgcagt cccaacctc caatcactca ccaacctctt gtcttccaat ttgtcctggc    360
tatcgctgga tgtgtctgcg gcgttttatc atattcctct tcattcctgct gctatgcctc    420
atcttcttgt tggttcttct ggactaccaa ggtatgttgc ccgtttgtcc tctacttcca    480
ggaacatcaa ccaccagcac ggggccatgc aagacctgca cgattcctgc tcaaggaacc    540
tctatgtttc cctcttggtg ctgtacaaaa ctttcggaca gaaactgcac ttgtattccc    600
atcccatcat cctgggcttt cgcaagattc ctatgggagt gggcctcagt ccgtttctcc    660
tggctcagtt tactagtgcc atttgttcag tggttcgtag ggctttcccc cactgtttgg    720
ctttcagtta tatggatgat gtggtattgg gggccaagtc tgtacaacat cttgagtccc    780
tttttacctc tattaccaat tttcttttgt ctttgggtat acatt                    825

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<210> 124

<211> 275

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 32-164 (G145R) + STR (serotype d) sequence

<400> 124

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Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1          5          10          15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
          20          25          30

Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro
          35          40          45

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
50          55          60

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
65          70          75          80

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sequence listing_ST25.txt

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
85 90 95

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
100 105 110

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
115 120 125

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
130 135 140

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
145 150 155 160

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
165 170 175

Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
180 185 190

Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
195 200 205

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
210 215 220

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
225 230 235 240

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
245 250 255

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
260 265 270

Val Tyr Ile
275

<210> 125
<211> 825
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 (Q129R/G145R)/STR-tag (serotype d) sequence

<400> 125

sequence listing_ST25.txt

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gaaaaagcgg ccgcccctgc accgaacatg gagaacacaa catcaggatt cctaggaccc    180
ctgctcgtgt tacaggcggg gtttttcttg ttgacaagaa tcctcacaat accacagagt    240
ctagactcgt ggtggacttc tctcaatttt ctagggggag caccacgtg tcctggccaa    300
aattcgcagt ccccaacctc caatcactca ccaacctctt gtcctccaat ttgtcctggc    360
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atcccatcat cctgggcttt cgcaagattc ctatgggagt gggcctcagt ccgtttctcc    660
tggtcagttt tactagtgcc atttgttcag tggttcgtag ggctttcccc cactgtttgg    720
ctttcagtta tatggatgat gtggtattgg gggccaagtc tgtacaacat cttgagttcc    780
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<210> 126

<211> 275

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 32-164 (Q129R/G145R)/STR-tag (serotype d) sequence

<400> 126

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
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Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
20 25 30

Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro
35 40 45

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
50 55 60

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
65 70 75 80

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
85 90 95

sequence listing_ST25.txt

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
100 105 110

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
115 120 125

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
130 135 140

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
145 150 155 160

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
165 170 175

Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
180 185 190

Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
195 200 205

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
210 215 220

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
225 230 235 240

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
245 250 255

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
260 265 270

Val Tyr Ile
275

<210> 127
<211> 1203
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 + ZZ (serotype d) sequence

<400> 127
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cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaacaat 120

ccagattggg gcggccgcgc gcaacacgat gaagccgtag acaacaaatt caacaaagaa 180
Page 113

sequence listing_ST25.txt

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aaaaagctaa atgatgctca ggcgccgaaa gtagacaaca aattcaacaa agaacaacaa 360
aacgcgttct atgagatctt acattttacct aacttaaacg aagaacaacg aaacgccttc 420
atccaaagtt taaaagatga cccaagccaa agcgctaacc ttttagcaga agctaaaaag 480
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att 1203

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<210> 128
 <211> 401
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 44-164 + ZZ (serotype d) sequence

<400> 128

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Ala Gln
 35 40 45

His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
 50 55 60

sequence listing_ST25.txt

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Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
65              70              75              80

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
85              90              95

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp
100             105             110

Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
115             120             125

Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu
130             135             140

Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys
145             150             155             160

Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn Met
165             170             175

Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala
180             185             190

Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp
195             200             205

Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro
210             215             220

Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys
225             230             235             240

Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile
245             250             255

Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu
260             265             270

Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr
275             280             285

Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln
290             295             300

Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly
305             310             315             320

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sequence listing_ST25.txt

Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe
325 330 335

Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val
340 345 350

Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser
355 360 365

Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu
370 375 380

Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr
385 390 395 400

Ile

<210> 129
<211> 1203
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 (Q129R) + ZZ (serotype d) sequence

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ccagattggg gcggccgcgc gcaacacgat gaagccgtag acaacaaatt caacaaagaa 180
caacaaaacg cgttctatga gatcttacat ttacctaact taaacgaaga acaacgaaac 240
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atccaaagtt taaaagatga cccaagccaa agcgctaacc ttttagcaga agctaaaaag 480
ctaaatgatg ctcaggcgcc gaaagcggcc gccctgcac cgaacatgga gaacacaaca 540
tcaggattcc taggaccctt gctcgtgtta caggcggggt ttttcttggt gacaagaatc 600
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cccacgtgtc ctggccaaaa ttcgcagtcc ccaacctcca atcactcacc aacctcttgt 720
cctccaattt gtcctggcta tcgctggatg tgtctgcggc gttttatcat attcctcttc 780
atcctgctgc tatgcctcat cttcttggtg gttcttctgg actaccaagg tatgttgccc 840

sequence listing_ST25.txt

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aactgcactt gtattcccat cccatcatcc tgggctttcg caagattcct atgggagtg    1020
gcctcagtcc gtttctcctg gctcagttta ctagtgccat ttgttcagtg gttcgtaggg    1080
ctttcccca ctgtttggct ttcagttata tggatgatgt ggtattgggg gccaaagtctg    1140
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att                                                                    1203

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<210> 130
 <211> 401
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 44-164 (Q129R) + ZZ (serotype d) sequence

<400> 130

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Ala Gln
 35 40 45

His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
 50 55 60

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
 65 70 75 80

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
 85 90 95

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp
 100 105 110

Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
 115 120 125

Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu
 130 135 140

Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys
 Page 117

sequence = string.strip("\n")

Page 118

sequence listing_ST25.txt

file

<210> 131
<211> 1203
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 (G145R) + ZZ (serotype d) sequence

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aaaaagctaa atgatgctca ggcgccgaaa gtagacaaca aattcaacaa agaacaacaa 360
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atccaaagtt taaaagatga cccaagccaa agcgctaacc ttttagcaga agctaaaaag 480
ctaaatgatg ctcaggcgcc gaaagcggcc gccctgcac cgaacatgga gaacacaaca 540
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ctcacaatac cacagagtct agactcgtgg tggacttctc tcaattttct agggggagca 660
cccacgtgtc ctggccaaaa ttgcagtc ccaacctcca atcactcacc aacctcttgt 720
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att 1203

<210> 132
<211> 401
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 44-164 (G145R) + ZZ (serotype d)

sequence listing_ST25.txt

sequence

<400> 132

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Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1      5      10     15
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20     25     30
Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Ala Gln
35     40     45
His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
50     55     60
Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
65     70     75     80
Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
85     90     95
Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp
100    105    110
Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
115    120    125
Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu
130    135    140
Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys
145    150    155    160
Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn Met
165    170    175
Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala
180    185    190
Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp
195    200    205
Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro
210    215    220
Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys
225    230    235    240

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sequence listing_ST25.txt

Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile
245 250 255

Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu
260 265 270

Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr
275 280 285

Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln
290 295 300

Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg
305 310 315 320

Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe
325 330 335

Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val
340 345 350

Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser
355 360 365

Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu
370 375 380

Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr
385 390 395 400

Ile

<210> 133

<211> 1203

<212> DNA

<213> artificial sequence

<220>

<223> 44-164 (Q129R/G145R) + ZZ (serotype d) sequence

<400> 133

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cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120

ccagattggg gcggccgcgc gcaacacgat gaagccgtag acaacaaatt caacaaagaa 180

caacaaaacg cggttctatga gatcttacat ttacctaact taaacgaaga acaacgaaac 240

gccttcatcc aaagtttaaa agatgaccca agccaaagcg ctaacctttt agcagaagct 300

sequence listing_ST25.txt

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aaaaagctaa atgatgctca ggcgccgaaa gtagacaaca aattcaacaa agaacaacaa   360
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atccaaagtt taaaagatga cccaagccaa agcgctaacc ttttagcaga agctaaaaag   480
ctaaatgatg ctcaggcgcc gaaagcggcc gccctgcac cgaacatgga gaacacaaca   540
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ctcacaatac cacagagtct agactcgtgg tggacttctc tcaattttct agggggagca   660
cccacgtgtc ctggccaaaa ttcgcagtcc ccaacctcca atcactcacc aacctcttgt   720
cctccaattt gtcctggcta tcgctggatg tgtctgcggc gttttatcat attcctcttc   780
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aactgcactt gtattcccat cccatcatcc tgggctttcg caagattcct atgggagtg   1020
gcctcagtcc gtttctcctg gctcagttta ctagtgccat ttgttcagtg gttcgtaggg   1080
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<210> 134

<211> 401

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 44-164 (Q129R/G145R) + ZZ (serotype d)
sequence

<400> 134

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Ala Gln
35 40 45

His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
50 55 60

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
65 70 75 80

sequence listing_ST25.txt

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
85 90 95

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp
100 105 110

Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
115 120 125

Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu
130 135 140

Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys
145 150 155 160

Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn Met
165 170 175

Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala
180 185 190

Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp
195 200 205

Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro
210 215 220

Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys
225 230 235 240

Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile
245 250 255

Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu
260 265 270

Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr
275 280 285

Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg
290 295 300

Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg
305 310 315 320

Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe
Page 123

sequence_listing_ST25.txt

325

330

335

Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val
340 345 350

Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser
355 360 365

Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu
370 375 380

Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr
385 390 395 400

Ile

<210> 135
<211> 1002
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 + EGF (serotype d) sequence

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ctcagtttac tagtgccatt tgttcagtgg ttcgtagggc tttccccac tgtttggctt 900
tcagttatat ggatgatgtg gtattggggg ccaagtctgt acaacatctt gagtcccttt 960

sequence listing_ST25.txt

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1002

<210> 136

<211> 334

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 44-164 + EGF (serotype d) sequence

<400> 136

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Met Asn
35 40 45

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
50 55 60

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
65 70 75 80

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
85 90 95

Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr
100 105 110

Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe
115 120 125

Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp
130 135 140

Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn
145 150 155 160

Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile
165 170 175

Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu
180 185 190

Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr
Page 125

sequence listing_ST25.txt
195 200 205

Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr
210 215 220

Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr Ser
225 230 235 240

Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr
245 250 255

Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu
260 265 270

Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val
275 280 285

Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp
290 295 300

Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe
305 310 315 320

Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
325 330

<210> 137
<211> 1002
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 (Q129R) + EGF (serotype d) sequence

<400> 137
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cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg gcggccgcat gaactctgat tccgaatgcc cgctgtctca tgacggttac 180
tgcttgcatt atggcgtatg catgtacatc gaagctctgg acaaatacgc atgcaactgt 240
gttgtaggtt acatcggcga acgttgccag tatcgcgacc tgaaatgggtg ggaactgcgt 300
aaggcggccg cccctgcacc gaacatggag aacacaacat caggattcct aggaccctg 360
ctcgtgttac aggcgggggtt tttcttggtg acaagaatcc tcacaatacc acagagtcta 420
gactcgtggt ggacttctct caattttcta gggggagcac ccacgtgtcc tggccaaaat 480
tcgcagtccc caacctccaa tcaactacca acctcttgtc ctccaatttg tcctggctat 540
cgctggatgt gtctgcggcg ttttatcata ttctcttcca tcctgctgct atgcctcatc 600

sequence listing_ST25.txt

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atgtttccct cttgttgctg tacaaaacct tcggacggaa actgcacttg tattcccatc 780
ccatcatcct gggctttcgc aagattccta tgggagtggg cctcagtccg tttctcctgg 840
ctcagtttac tagtgccatt tgttcagtgg ttcgtagggc tttccccac tgtttggtt 900
tcagttatat ggatgatgtg gtattggggg ccaagtctgt acaacatctt gagtcccttt 960
ttacctctat taccaatttt cttttgtctt tgggtataca tt 1002

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<210> 138
 <211> 334
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 44-164 (Q129R) + EGF (serotype d)
 sequence

<400> 138

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Met Asn
 35 40 45

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
 50 55 60

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
 65 70 75 80

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
 85 90 95

Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr
 100 105 110

Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe
 115 120 125

Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp
 130 135 140

sequence listing_ST25.txt

Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn
145 150 155 160

Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile
165 170 175

Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu
180 185 190

Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr
195 200 205

Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr
210 215 220

Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr Ser
225 230 235 240

Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr
245 250 255

Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu
260 265 270

Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val
275 280 285

Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp
290 295 300

Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe
305 310 315 320

Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
325 330

<210> 139
<211> 1002
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 (G145R) + EGF (serotype d) sequence

<400> 139
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cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaacaat 120
ccagattggg gcggccgcga gaactctgat tccgaatgcc cgctgtctca tgacgggttac 180

sequence listing_ST25.txt

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tgctgcatg atggcgtatg catgtacatc gaagctctgg acaatacgc atgcaactgt 240
gtttaggtt acatcggcga acgttgccag tatcgcgacc tgaaatggtg ggaactgcgt 300
aaggcggccg cccctgcacc gaacatggag aacacaacat caggattcct aggaccctg 360
ctcgtgttac aggcggggtt tttcttggtg acaagaatcc tcacaatacc acagagtcta 420
gactcgtggt ggactttctt caattttcta gggggagcac ccacgtgtcc tggccaaaat 480
tcgcagtccc caacctcaa tcactcacca acctcttgtc ctccaatttg tcctggctat 540
cgctggatgt gtctgcggcg ttttatcata ttctcttca tcctgctgct atgcctcatc 600
ttcttggttg ttcttctgga ctaccaaggt atgttgcccg ttgtcctct acttccagga 660
acatcaacca ccagcacggg gccatgcaag acctgcacga ttctgctca aggaacctct 720
atgtttccct cttgttgctg taaaaacct tcggacagaa actgcacttg tattcccatc 780
ccatcatcct gggctttcgc aagattccta tgggagtggg cctcagtccg tttctcctgg 840
ctcagtttac tagtgccatt tgttcagtgg ttcgtagggc tttccccac tgtttggtt 900
tcagttatat ggatgatgtg gtattggggg ccaagtctgt acaacatctt gagtccttt 960
ttaccttat taccaatttt cttttgtctt tgggtatata tt 1002

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<210> 140

<211> 334

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 44-164 (G145R) + EGF (serotype d)
sequence

<400> 140

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Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1           5           10           15

```

```

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20           25           30

```

```

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Met Asn
35           40           45

```

```

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
50           55           60

```

```

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
65           70           75           80

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```

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
85           90           95

```

sequence listing_ST25.txt

Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr
100 105 110

Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe
115 120 125

Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp
130 135 140

Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn
145 150 155 160

Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile
165 170 175

Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu
180 185 190

Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr
195 200 205

Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr
210 215 220

Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr Ser
225 230 235 240

Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys Thr
245 250 255

Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu
260 265 270

Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val
275 280 285

Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp
290 295 300

Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe
305 310 315 320

Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
325 330

<210> 141
<211> 1002

sequence listing_ST25.txt

<212> DNA

<213> artificial sequence

<220>

<223> 44-164 (Q129R/G145R) + EGF (serotype d) sequence

<400> 141

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ccagattggg  gcggccgcat gaactctgat tccgaatgcc cgctgtctca tgacggttac    180
tgcctgcatg  atggcgtatg catgtacatc gaagctctgg acaaatacgc atgcaactgt    240
gttgtagggt  acatcggcga acgttgccag tatcgcgacc tgaaatggtg ggaactgcgt    300
aaggcggccg  cccctgcacc gaacatggag aacacaacat caggattcct aggaccctg    360
ctcgtgttac  aggcgggggtt tttcttggtg acaagaatcc tcacaatacc acagagtcta    420
gactcgtggt  ggacttctct caattttcta gggggagcac ccacgtgtcc tggccaaaat    480
tcgcagtccc  caacctccaa tcactcacca acctcttgtc ctccaatttg tcctggctat    540
cgctggatgt  gtctgcggcg ttttatcata ttctcttca tcctgctgct atgcctcatc    600
ttcttggttg  ttcttctgga ctaccaaggt atgttgcccg ttgtctctct acttccagga    660
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atgtttccct  cttgttgctg taaaaaacct tcggacagaa actgcacttg tattcccatc    780
ccatcatcct  gggctttcgc aagattccta tgggagtggg cctcagtccg tttctcctgg    840
ctcagtttac  tagtgccatt tgttcagtgg ttcgtagggc tttccccac tgtttgctt    900
tcagttatat  ggatgatgtg gtattggggg ccaagtctgt acaacatctt gagtccttt    960
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<210> 142

<211> 334

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 44-164 (Q129R/G145R) + EGF (serotype d) sequence

<400> 142

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Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1          5          10          15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
          20          25          30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Met Asn
          35          40          45
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sequence_listing_ST25.txt

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
50 55 60

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
65 70 75 80

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
85 90 95

Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr
100 105 110

Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe
115 120 125

Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp
130 135 140

Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn
145 150 155 160

Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile
165 170 175

Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu
180 185 190

Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr
195 200 205

Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr
210 215 220

Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr Ser
225 230 235 240

Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys Thr
245 250 255

Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu
260 265 270

Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val
275 280 285

Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp

sequence listing_ST25.txt

290

295

300

Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe
305 310 315 320

Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
325 330

<210> 143
<211> 861
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 + STR-tag (serotype d) sequence

<400> 143
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cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg gcggccgctg gagccacccg cagttcgaaa aagcggccgc ccctgcaccg 180
aacatggaga acacaacatc aggattccta ggacccctgc tcgtgttaca ggcgggggtt 240
ttcttggtga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc 300
aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcccc aacctccaat 360
cactcacaa cctcttgctc tccaatttgt cctggctatc gctggatgtg tctgcggcgt 420
tttatcatat tcctcttcat cctgctgcta tgcctcatct tcttggttgt tcttctggac 480
taccaaggta tggtgccgct ttgtcctcta cttccaggaa catcaaccac cagcacgggg 540
ccatgcaaga cctgcacgat tcctgtccta ggaacctcta tgtttcctc ttgttgctgt 600
acaaaacctt cggacggaaa ctgcatttgt attcccatcc catcatcctg ggctttcgca 660
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gttcagtgtg tcgtagggct ttccccact gtttggtctt cagttatatg gatgatgtgg 780
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<210> 144
<211> 287
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 44-164 + STR-tag (serotype d) sequence

<400> 144

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

sequence listing_ST25.txt

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Trp Ser
35 40 45

His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
50 55 60

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
65 70 75 80

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
85 90 95

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
100 105 110

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
115 120 125

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
130 135 140

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
145 150 155 160

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
165 170 175

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr
180 185 190

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys
195 200 205

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
210 215 220

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
225 230 235 240

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
245 250 255

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro

260

Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
275 280 285

<210> 145
<211> 861
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 (Q129R) + STR-tag (serotype d) sequence

<400> 145
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cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg gcggccgctg gagccacccg cagttcgaaa aagcggccgc ccctgcaccg 180
aacatggaga acacaacatc aggattccta ggacccctgc tcgtgttaca ggcgggggtt 240
ttcttgttga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc 300
aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcccc aacctccaat 360
cactcaccaa cctcttgtcc tccaatttgt cctggctatc gctggatgtg tctgcggcgt 420
tttatcatat tcctcttcat cctgctgcta tgcctcatct tcttgttggt tcttctggac 480
taccaaggta tggtgcccgt ttgtcctcta cttccaggaa catcaaccac cagcacgggg 540
ccatgcaaga cctgcacgat tcctgctcga ggaacctcta tgtttccctc ttggtgctgt 600
acaaaacctt cggacggaaa ctgcatttgt attcccatcc catcatcctg ggctttcgca 660
agattcctat gggagtgggc ctgagtcctg ttctcctggc tcagtttact agtgccattt 720
gttcagtggg tcgtagggct ttccccact gtttggtttt cagttatatg gatgatgtgg 780
tattgggggc caagtctgta caacatcttg agtccctttt tacctctatt accaattttc 840
ttttgtcttt gggatacat t 861

<210> 146
<211> 287
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 44-164 (Q129R) + STR-tag (serotype d) sequence

<400> 146

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
Page 135

sequence listing_ST25.txt

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20
25
30
Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Trp Ser
35 40 45
His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
50 55 60
Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
65 70 75 80
Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
85 90 95
Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
100 105 110
Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
115 120 125
Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
130 135 140
Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
145 150 155 160
Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
165 170 175
Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr
180 185 190
Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys
195 200 205
Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
210 215 220
Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
225 230 235 240
Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
245 250 255
Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
260 265 270

```


sequence listing_ST25.txt

Phe	Leu	Pro	Leu	Leu	Pro	Ile	Phe	Phe	Cys	Leu	Trp	Val	Tyr	Ile
	275						280					285		

<210> 147
 <211> 861
 <212> DNA
 <213> artificial sequence

<220>
 <223> 44-164 (G145R) + STR-tag (serotype d) sequence

<400> 147

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cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat	120
ccagattggg gcggccgctg gagccacccg cagttcgaaa aagcggccgc ccctgcaccg	180
aacatggaga acacaacatc aggattccta ggaccctcgc tcgtgttaca ggcgggggtt	240
ttcttggtga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc	300
aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcccc aacctccaat	360
cactcaccaa cctcttgtcc tccaatttgt cctggctatc gctggatgtg tctgcggcgt	420
tttatcatat tcctcttcat cctgctgcta tgcctcatct tcttggtggt tcttctggac	480
taccaaggta tggtgcccgt ttgtcctcta cttccaggaa catcaaccac cagcacgggg	540
ccatgcaaga cctgcacgat tcctgctcaa ggaacctcta tgtttccctc ttggtgctgt	600
acaaaacctt cggacagaaa ctgcacttgt attcccatcc catcatcctg ggctttcgca	660
agattcctat gggagtgggc ctgagtcctt ttctcctggc tcagtttact agtgccattt	720
gttcagtggg tcgtagggct ttccccact gtttggtctt cagttatatg gatgatgtgg	780
tattgggggc caagtctgta caacatcttg agtccctttt tacctctatt accaattttc	840
ttttgtcttt gggatacat t	861

<210> 148
 <211> 286
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 44-164 (G145R) + STR-tag (serotype d) sequence

<400> 148

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Lys	Gly	Met	Gly	Thr	Asn	Leu
1				5					10					15	

Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro
			20					25					30		

sequence listing_ST25.txt

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Trp Ser
35 40 45

His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
50 55 60

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
65 70 75 80

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
85 90 95

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
100 105 110

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
115 120 125

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
130 135 140

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
145 150 155 160

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
165 170 175

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr
180 185 190

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys
195 200 205

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
210 215 220

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
225 230 235 240

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
245 250 255

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
260 265 270

Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr
275 280 285

sequence listing_ST25.txt

<210> 149
 <211> 861
 <212> DNA
 <213> artificial sequence

<220>
 <223> 44-164 (Q129R/G145R) + STR-tag (serotype d) sequence

<400> 149
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 cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
 ccagattggg gcggccgctg gagccacccg cagttcgaaa aagcggccgc ccctgcaccg 180
 aacatggaga acacaacatc aggattccta ggacccctgc tcgtgttaca ggcgggggtt 240
 ttcttgttga caagaatcct cacaatacca cagagtctag actcgtgggtg gacttctctc 300
 aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcccc aacctccaat 360
 cactcaccaa cctcttgtcc tccaatttgt cctggctatc gctggatgtg tctgcggcgt 420
 tttatcatat tcctcttcat cctgctgcta tgcctcatct tcttggtggt tcttctggac 480
 taccaaggta tgttgcccgt ttgtcctcta cttccaggaa catcaaccac cagcacgggg 540
 ccatgcaaga cctgcacgat tcctgctcga ggaacctcta tgtttccttc ttggtgctgt 600
 acaaaacctt cggacagaaa ctgcatttgt attcccatcc catcatcctg ggctttcgca 660
 agattcctat gggagtgggc ctgagtcctg ttctcctggc tcagtttact agtgccattt 720
 gttcagtggg tcgtagggct ttccccact gtttggtttt cagttatatg gatgatgtgg 780
 tattgggggc caagtctgta caacatcttg agtccctttt tacctctatt accaattttc 840
 ttttgtcttt gggtatacat t 861

<210> 150
 <211> 287
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 44-164 (Q129R/G145R) + STR-tag
 (serotype d) sequence

<400> 150

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15
 Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30
 Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Trp Ser
 35 40 45

sequence listing_ST25.txt

His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
50 55 60

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
65 70 75 80

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
85 90 95

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
100 105 110

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
115 120 125

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
130 135 140

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
145 150 155 160

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
165 170 175

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr
180 185 190

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys
195 200 205

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
210 215 220

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
225 230 235 240

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
245 250 255

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
260 265 270

Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
275 280 285

<210> 151
<211> 1254

sequence listing_ST25.txt

<212> DNA

<213> artificial sequence

<220>

<223> 61-164 + ZZ (serotype d) sequence

<400> 151

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cctctgggat  tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat    120
ccagattggg  acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg    180
ggcggccgcg  cgcaacacga tgaagccgta gacaacaaat tcaacaaaga acaacaaaac    240
gcgttctatg  agatcttaca tttacctaac ttaaacgaag aacaacgaaa cgccttcac    300
caaagttaa  aagatgaccc aagccaaagc gctaaccttt tagcagaagc taaaaagcta    360
aatgatgctc  aggcgccgaa agtagacaac aaattcaaca aagaacaaca aaacgcgttc    420
tatgagatct  tacatttacc taacttaaac gaagaacaac gaaacgcctt catccaaagt    480
ttaaagatg  acccaagcca aagcgctaac ctttttagcag aagctaaaaa gctaaatgat    540
gctcaggcgc  cgaaagcggc cgcccctgca ccgaacatgg agaacacaac atcaggattc    600
ctaggacccc  tgctcgtggt acaggcgggg tttttcttgt tgacaagaat cctcacaata    660
ccacagagtc  tagactcgtg gtggacttct ctcaattttc tagggggagc acccacgtgt    720
cctggccaaa  attcgcagtc cccaacctcc aatcactcac caacctcttg tcctccaatt    780
tgtcctggct  atcgctggat gtgtctgcgg cgttttatca tattcctctt catcctgctg    840
ctatgcctca  tcttcttggt ggttcttctg gactaccaag gtatgttgcc cgtttgcct    900
ctacttcag  gaacatcaac caccagcacg gggccatgca agacctgcac gattcctgct    960
caaggaacct  ctatgtttcc ctcttgttgc tgtacaaaac cttcggacgg aaactgcact   1020
tgtattccca  tcccatcatc ctgggctttc gcaagattcc tatgggagtg ggcctcagtc   1080
cgtttctcct  ggctcagttt actagtacca tttgttcagt ggttcgtagg gctttccccc   1140
actgtttggc  tttcagttat atggatgatg tggatattgg ggccaagtct gtacaacatc   1200
ttgagtcctt  ttttacctct attaccaatt ttcttttctc tttgggtata catt       1254

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<210> 152

<211> 418

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 61-164 + ZZ (serotype d) sequence

<400> 152

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Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1           5           10           15

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sequence listing_ST25.txt

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Ala
50 55 60

Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn
65 70 75 80

Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg
85 90 95

Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
100 105 110

Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val
115 120 125

Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
130 135 140

His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser
145 150 155 160

Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
165 170 175

Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn
180 185 190

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
195 200 205

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
210 215 220

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
225 230 235 240

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
245 250 255

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
260 265 270

sequence listing_ST25.txt

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
275 280 285
Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
290 295 300
Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
305 310 315 320
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
325 330 335
Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
340 345 350
Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
355 360 365
Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
370 375 380
Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
385 390 395 400
Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
405 410 415

Tyr Ile

<210> 153
<211> 1254
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 (Q129R) + ZZ (serotype d) sequence

<400> 153
atgggaggtt ggtcttccaa acctcggaag ggcattggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgcg cgcaacacga tgaagccgta gacaacaaat tcaacaaaga acaacaaaac 240
gcgttctatg agatcttaca ttacctaac ttaaacgaag aacaacgaaa cgccttcac 300
caaagtttaa aagatgaccc aagccaaagc gctaaccttt tagcagaagc taaaaagcta 360

sequence listing_ST25.txt

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aatgatgctc aggcgccgaa agtagacaac aaattcaaca aagaacaaca aaacgcgttc 420
tatgagatct tacatttacc taacttaaac gaagaacaac gaaacgcctt catccaaagt 480
ttaaagatg acccaagcca aagcgctaac ctttttagcag aagctaaaaa gctaaatgat 540
gctcaggcgc cgaaagcggc cgcccctgca ccgaacatgg agaacacaac atcaggattc 600
ctaggacccc tgctcgtggt acaggcgggg tttttcttgt tgacaagaat cctcacaata 660
ccacagagtc tagactcgtg gtggacttct ctcaattttc tagggggagc acccacgtgt 720
cctggccaaa attcgcagtc cccaacctcc aatcactcac caacctcttg tcctccaatt 780
tgtcctggct atcgctggat gtgtctgcgg cgttttatca ttttctctt catcctgctg 840
ctatgcctca tcttcttggt ggttcttctg gactaccaag gtatgttgcc cgtttgcct 900
ctacttcag gaacatcaac caccagcacg gggccatgca agacctgcac gattcctgct 960
cgaggaacct ctatgtttcc ctcttgttgc tgtacaaaac cttcggacgg aaactgcact 1020
tgtattccca tcccatcatc ctgggctttc gcaagattcc tatgggagtg ggcctcagtc 1080
cgtttctcct ggctcagttt actagtgcc tttgttcagt ggttcgtagg gctttcccc 1140
actgtttggc tttcagttat atggatgatg tgggtattgg ggccaagtct gtacaacatc 1200
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<210> 154
 <211> 418
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 61-164 (Q129R) + ZZ (serotype d) sequence

<400> 154

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Ala
 50 55 60

Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn
 65 70 75 80

Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg
 Page 144

sequence listing_ST25.txt

85

90

95

```

Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
100      105      110

Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val
115      120      125

Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
130      135      140

His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser
145      150      155      160

Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
165      170      175

Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn
180      185      190

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
195      200      205

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
210      215      220

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
225      230      235      240

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
245      250      255

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
260      265      270

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
275      280      285

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
290      295      300

Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
305      310      315      320

Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
325      330      335

```

sequence listing_ST25.txt

Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
 340 345 350

Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
 355 360 365

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
 370 375 380

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
 385 390 395 400

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
 405 410 415

Tyr Ile

<210> 155
 <211> 1254
 <212> DNA
 <213> artificial sequence

<220>
 <223> 61-164 (G145R) + ZZ (serotype d) sequence

<400> 155
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 cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaacaat 120
 ccagattggg acttcaacc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
 ggcgccgcg cgcaacacga tgaagccgta gacaacaaat tcaacaaaga acaacaaaac 240
 gcgttctatg agatcttaca ttacctaac ttaaacgaag aacaacgaaa cgccttcac 300
 caaagttaa aagatgacc aagccaaagc gctaaccttt tagcagaagc taaaaagcta 360
 aatgatgctc aggcgccgaa agtagacaac aaattcaaca agaacaaca aaacgcgttc 420
 tatgagatct tacatttacc taacttaaac gaagaacaac gaaacgcctt catccaaagt 480
 ttaaaagatg acccaagcca aagcgctaac cttttagcag aagctaaaaa gctaaatgat 540
 gctcaggcgc cgaaagcggc cgcccctgca ccgaacatgg agaacacaac atcaggattc 600
 ctaggacccc tgctcgtgtt acaggcgggg tttttcttgt tgacaagaat cctcacaata 660
 ccacagagtc tagactcgtg gtggacttct ctcaattttc tagggggagc acccagtggt 720
 cctggccaaa attcgcagtc cccaacctcc aatcactcac caacctcttg tcctccaatt 780
 tgcctgggt atcgctggat gtgtctgcgg cgttttatca tattcctctt catcctgctg 840
 ctatgcctca tcttcttggt ggttcttctg gactaccaag gtatgttgcc cgtttgctct 900

sequence listing_ST25.txt

```
ctactttccag gaacatcaac caccagcacg gggccatgca agacctgcac gattcctgct    960
caaggaacct ctatgtttcc ctcttgttgc tgtacaaaac cttcggacag aaactgcact    1020
tgtattccca tcccatcatc ctgggctttc gcaagattcc tatgggagtg ggcctcagtc    1080
cgttttctct ggctcagttt actagtgcc tttgttcagt ggttcgtagg gctttccccc    1140
actgtttggc tttcagttat atggatgatg tgggtattggg ggccaagtct gtacaacatc    1200
ttgagtcctt tttacctct attaccaatt ttcttttgtc tttgggtata catt          1254
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<210> 156

<211> 418

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 61-164 (G145R) + ZZ (serotype d) sequence

<400> 156

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Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1          5          10          15
```

```
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
          20          25          30
```

```
Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
          35          40          45
```

```
Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Ala
          50          55          60
```

```
Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn
          65          70          75          80
```

```
Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg
          85          90          95
```

```
Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
          100          105          110
```

```
Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val
          115          120          125
```

```
Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
          130          135          140
```

```
His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser
          145          150          155          160
```

sequence listing_ST25.txt

```

Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
    165                      170                      175

Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn
    180                      185                      190

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
    195                      200                      205

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
    210                      215                      220

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
    225                      230                      235                      240

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
    245                      250                      255

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
    260                      265                      270

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
    275                      280                      285

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
    290                      295                      300

Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
    305                      310                      315                      320

Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
    325                      330                      335

Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
    340                      345                      350

Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
    355                      360                      365

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
    370                      375                      380

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
    385                      390                      395                      400

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
    405                      410                      415

```

sequence listing_ST25.txt

Tyr Ile

<210> 157
<211> 1254
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 (Q129R/G145R) + ZZ (serotype d) sequence

<400> 157
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cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgcg cgcaacacga tgaagccgta gacaacaaat tcaacaaaga acaacaaaac 240
gcgttctatg agatcttaca ttacctaac ttaaacgaag aacaacgaaa cgccttcatt 300
caaagttaa aagatgacct aagccaaagc gctaaccttt tagcagaagc taaaaagcta 360
aatgatgctc aggcgcgcaa agtagacaac aaattcaaca aagaacaaca aaacgcgttc 420
tatgagatct tacatttacc taacttaaac gaagaacaac gaaacgcctt catccaaagt 480
ttaaagatg acccaagcca aagcgctaac ctttttagcag aagctaaaaa gctaaatgat 540
gtcaggcgcg cgaaagcggc cgcccctgca ccgaacatgg agaacacaac atcaggattc 600
ctaggacccc tgctcgtgtt acaggcgggg tttttcttgt tgacaagaat cctcacaata 660
ccacagagtc tagactcgtg gtggacttct ctcaattttc tagggggagc acccacgtgt 720
cctggccaaa attcgcagtc cccaacctcc aatcactcac caacctcttg tctccaatt 780
tgtcctggct atcgtctgat gtgtctgcgg cgttttatca tattcctctt catcctgctg 840
ctatgcctca tcttcttggt ggttcttctg gactaccaag gtatgttgcc cgtttgtcct 900
ctacttcag gaacatcaac caccagcacg gggccatgca agacctgcac gattcctgct 960
cgaggaacct ctatgtttcc ctcttggtgc tgtacaaaac cttcggacag aaactgcact 1020
tgtattccca tcccatcatc ctgggctttc gcaagattcc tatgggagtg ggcctcagtc 1080
cgtttctcct ggctcagttt actagtgcc tttgttcagt ggttcgtagg gctttcccc 1140
actgtttggc tttcagttat atggatgatg tggattggg ggccaagtct gtacaacatc 1200
ttgagtcctt tttacctct attaccaatt ttctttgtc tttgggtata catt 1254

<210> 158
<211> 418
<212> PRT
<213> artificial sequence

sequence listing_ST25.txt

<220>

<223> Proteins corresponding to 61-164 (Q129R/G145R) + ZZ (serotype d)
sequence

<400> 158

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Ala
50 55 60

Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn
65 70 75 80

Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg
85 90 95

Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
100 105 110

Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val
115 120 125

Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
130 135 140

His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser
145 150 155 160

Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
165 170 175

Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn
180 185 190

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
195 200 205

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
210 215 220

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
Page 150

sequence listing_ST25.txt

225 230 235 240

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
245 250 255

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
260 265 270

Ile Ile Phe Leu Phe Ile Leu Leu Cys Leu Ile Phe Leu Leu Val
275 280 285

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
290 295 300

Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
305 310 315 320

Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
325 330 335

Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
340 345 350

Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
355 360 365

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
370 375 380

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
385 390 395 400

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
405 410 415

Tyr Ile

<210> 159
<211> 1053
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 + EGF (serotype d) sequence

<400> 159
atgggagggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60

cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaacaat 120
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sequence_listing_ST25.txt

```

ccagattggg acttcaaccc caacaaggat caatggccag aggcaaata ggtaggagcg 180
ggcggccgca tgaactctga ttccgaatgc ccgctgtctc atgacggtta ctgcctgcat 240
gatggcgtat gcatgtacat cgaagctctg gacaaatacg catgcaactg tgttgtaggt 300
tacatcggcg aacgttgcca gtatcgcgac ctgaaatggg gggaactgcg taaggcggcc 360
gcccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta 420
caggcggggg ttttcttggt gacaagaatc ctcacaatac cacagagtct agactcgtgg 480
tggacttctc tcaattttct agggggagca cccacgtgtc ctggccaaaa ttcgcagtcc 540
ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 600
tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttggtg 660
gttcttctgg actaccaagg tatgttgccc gtttgtcctc tacttccagg aacatcaacc 720
accagcacgg ggccatgcaa gacctgcacg attcctgctc aaggaacctc tatgtttccc 780
tcttggtgct gtacaaaacc ttcggacgga aactgcactt gtattcccat cccatcatcc 840
tgggctttcg caagattcct atgggagtg gacctcagtcc gtttctcctg gctcagttta 900
ctagtgccat ttgttcagt gttcgtaggg ctttccccca ctgtttggct ttcagttata 960
tggatgatgt ggtattgggg gccaaagtctg tacaacatct tgagtccttt tttacctcta 1020
ttaccaattt tcttttgtct ttgggtatac att 1053

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<210> 160

<211> 351

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 61-164 + EGF (serotype d) sequence

<400> 160

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Met
50 55 60

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
65 70 75 80

sequence listing_ST25.txt

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
85 90 95

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
100 105 110

Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
115 120 125

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
130 135 140

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
145 150 155 160

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
165 170 175

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
180 185 190

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
195 200 205

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
210 215 220

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
225 230 235 240

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr
245 250 255

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys
260 265 270

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
275 280 285

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
290 295 300

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
305 310 315 320

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
325 330 335

sequence listing_ST25.txt

Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
 340 345 350

<210> 161
 <211> 1053
 <212> DNA
 <213> artificial sequence

<220>
 <223> 61-164 (Q129R) + EGF (serotype d) sequence

<400> 161
 atgggaggtt ggtcttccaa acctcggaaa ggcattggga cgaatctttc tgttcccaat 60
 cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
 ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
 ggcggccgca tgaactctga ttccgaatgc ccgctgtctc atgacggtta ctgcctgcat 240
 gatggcgtat gcatgtacat cgaagctctg gacaaatacg catgcaactg tgttgtaggt 300
 tacatcggcg aacgttgcca gtatcgcgac ctgaaatggt gggaactgcg taaggcggcc 360
 gccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta 420
 caggcggggg ttttcttggt gacaagaatc ctcacaatac cacagagtct agactcgtgg 480
 tggacttctc tcaattttct agggggagca cccacgtgtc ctggccaaaa ttcgcagtcc 540
 ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 600
 tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttggtg 660
 gttcttcttg actaccaagg tatgttgccc gtttgcctc tacttccagg aacatcaacc 720
 accagcacgg ggccatgcaa gacctgcacg attcctgctc gaggaacctc tatgtttccc 780
 tcttggtgct gtacaaaacc ttcggacgga aactgcactt gtattcccat cccatcatcc 840
 tgggctttcg caagattcct atgggagtg gacctcagtc gtttctcctg gctcagttta 900
 ctagtgccat ttgttcagtg gttcgtaggg ctttccccca ctgtttggct ttcagttata 960
 tggatgatgt ggtattgggg gccaaagtctg tacaacatct tgagtccttt ttacctcta 1020
 ttaccaattt tcttttgtct ttgggtatac att 1053

<210> 162
 <211> 351
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 61-164 (Q129R) + EGF (serotype d) sequence

<400> 162

sequence_listing_ST25.txt

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Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1      5      10      15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
      20      25      30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
      35      40      45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Met
      50      55      60

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
      65      70      75      80

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
      85      90      95

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
      100      105      110

Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
      115      120      125

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
      130      135      140

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
      145      150      155      160

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
      165      170      175

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
      180      185      190

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
      195      200      205

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
      210      215      220

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
      225      230      235      240

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr
      245      250      255

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sequence listing_ST25.txt

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys
260 265 270

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
275 280 285

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
290 295 300

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
305 310 315 320

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
325 330 335

Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
340 345 350

<210> 163
<211> 1053
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 (G145R) + EGF (serotype d) sequence

<400> 163
atgggaggtt ggtcttccaa acctcgga aa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgca tgaactctga ttccgaatgc ccgctgtctc atgacgggta ctgcctgcat 240
gatggcgtat gcatgtacat cgaagctctg gacaaatacg catgcaactg tgttgtaggt 300
tacatcggcg aacgttgcca gtatcgcgac ctgaaatggg gggaactgcg taaggcggcc 360
gccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta 420
caggcggggg ttttcttggt gacaagaatc ctcaataac cacagagtct agactcgtgg 480
tggaattctc tcaattttct agggggagca ccacgtgtc ctggccaaaa ttcgcagtcc 540
ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 600
tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttggtg 660
gttcttctgg actaccaagg tatgttgccc gtttgctctc tacttccagg aacatcaacc 720
accagcacgg ggccatgcaa gacctgcacg attcctgctc aaggaacctc tatgtttccc 780
tcttggtgct gtacaaaacc ttcggacaga aactgcactt gtattcccat cccatcatcc 840
tgggctttcg caagattcct atgggagtg gacctagtc gtttctcctg gctcagttta 900

sequence listing_ST25.txt

ctagtgccat ttgttcagtg gttcgtaggg ctttcccca ctgtttggct ttcagttata 960
 tggatgatgt ggtattgggg gccaaagtctg tacaacatct tgagtcctt tttacctcta 1020
 ttaccaattt tcttttgtct ttgggtatac att 1053

<210> 164
 <211> 351
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to61-164 (G145R) + EGF (serotype d)
 sequence

<400> 164

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Met
 50 55 60

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
 65 70 75 80

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
 85 90 95

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
 100 105 110

Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
 115 120 125

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
 130 135 140

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
 145 150 155 160

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
 165 170 175

sequence listing_ST25.txt

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
180 185 190

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
195 200 205

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
210 215 220

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
225 230 235 240

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr
245 250 255

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys
260 265 270

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
275 280 285

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
290 295 300

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
305 310 315 320

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
325 330 335

Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
340 345 350

<210> 165
<211> 1053
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 (Q129R/G145R) + EGF (serotype d) sequence

<400> 165
atgggagggtt ggtcttccaa acctcgga aa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaacaat 120
ccagattggg acttcaacc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgca tgaactctga ttccgaatgc ccgctgtctc atgacggtta ctgcctgcat 240
gatggcgtat gcatgtacat cgaagctctg gacaaatagc catgcaactg tgttgtaggt 300

sequence listing_ST25.txt

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tacatcggcg aacgttgcca gtatcgcgac ctgaaatggt gggaactgcg taaggcggcc 360
gccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta 420
caggcgggggt ttttcttgtt gacaagaatc ctcacaatac cacagagtct agactcgtgg 480
tggacttctc tcaattttct agggggagca cccacgtgtc ctggccaaaa ttcgcagtcc 540
ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 600
tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttgttg 660
gttcttctgg actaccaagg tatgttgccc gtttgcctc tacttccagg aacatcaacc 720
accagcacgg ggccatgcaa gacctgcacg attcctgtc gaggaacctc tatgtttccc 780
tcttgttgct gtacaaaacc ttcggacaga aactgcactt gtattcccat cccatcatcc 840
tgggctttcg caagattcct atgggagtg gctcagtc gtttctcctg gctcagttta 900
ctagtccat ttgttcagtg gttcgtagg ctttcccca ctgtttggct ttcagttata 960
tggatgatgt ggtattgggg gccaaagtctg tacaacatct tgagtcctt tttacctcta 1020
ttaccaattt tcttttgtct ttgggtatac att 1053
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<210> 166

<211> 351

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 61-164 (Q129R/G145R) + EGF (serotype d) sequence

<400> 166

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Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1          5          10          15
```

```
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
          20          25          30
```

```
Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
          35          40          45
```

```
Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Met
          50          55          60
```

```
Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
          65          70          75          80
```

```
Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
          85          90          95
```

```
Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
          100          105          110          115          120          125          130          135          140          145          150          155          160          165          170          175          180          185          190          195          200          205          210          215          220          225          230          235          240          245          250          255          260          265          270          275          280          285          290          295          300          305          310          315          320          325          330          335          340          345          350          355          360          365          370          375          380          385          390          395          400          405          410          415          420          425          430          435          440          445          450          455          460          465          470          475          480          485          490          495          500          505          510          515          520          525          530          535          540          545          550          555          560          565          570          575          580          585          590          595          600          605          610          615          620          625          630          635          640          645          650          655          660          665          670          675          680          685          690          695          700          705          710          715          720          725          730          735          740          745          750          755          760          765          770          775          780          785          790          795          800          805          810          815          820          825          830          835          840          845          850          855          860          865          870          875          880          885          890          895          900          905          910          915          920          925          930          935          940          945          950          955          960          965          970          975          980          985          990          995          1000
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sequence listing_ST25.txt

100																	
Trp	Trp	Glu	Leu	Arg	Lys	Ala	Ala	Ala	Pro	Ala	Pro	Asn	Met	Glu	Asn		
		115					120					125					
Thr	Thr	Ser	Gly	Phe	Leu	Gly	Pro	Leu	Leu	Val	Leu	Gln	Ala	Gly	Phe		
	130					135					140						
Phe	Leu	Leu	Thr	Arg	Ile	Leu	Thr	Ile	Pro	Gln	Ser	Leu	Asp	Ser	Trp		
145					150					155					160		
Trp	Thr	Ser	Leu	Asn	Phe	Leu	Gly	Gly	Ala	Pro	Thr	Cys	Pro	Gly	Gln		
				165					170					175			
Asn	Ser	Gln	Ser	Pro	Thr	Ser	Asn	His	Ser	Pro	Thr	Ser	Cys	Pro	Pro		
			180					185					190				
Ile	Cys	Pro	Gly	Tyr	Arg	Trp	Met	Cys	Leu	Arg	Arg	Phe	Ile	Ile	Phe		
		195					200					205					
Leu	Phe	Ile	Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp		
	210					215						220					
Tyr	Gln	Gly	Met	Leu	Pro	Val	Cys	Pro	Leu	Leu	Pro	Gly	Thr	Ser	Thr		
225					230					235					240		
Thr	Ser	Thr	Gly	Pro	Cys	Lys	Thr	Cys	Thr	Ile	Pro	Ala	Arg	Gly	Thr		
				245					250					255			
Ser	Met	Phe	Pro	Ser	Cys	Cys	Cys	Thr	Lys	Pro	Ser	Asp	Arg	Asn	Cys		
			260					265					270				
Thr	Cys	Ile	Pro	Ile	Pro	Ser	Ser	Trp	Ala	Phe	Ala	Arg	Phe	Leu	Trp		
		275					280					285					
Glu	Trp	Ala	Ser	Val	Arg	Phe	Ser	Trp	Leu	Ser	Leu	Leu	Val	Pro	Phe		
	290					295					300						
Val	Gln	Trp	Phe	Val	Gly	Leu	Ser	Pro	Thr	Val	Trp	Leu	Ser	Val	Ile		
305					310					315					320		
Trp	Met	Met	Trp	Tyr	Trp	Gly	Pro	Ser	Leu	Tyr	Asn	Ile	Leu	Ser	Pro		
				325					330					335			
Phe	Leu	Pro	Leu	Leu	Pro	Ile	Phe	Phe	Cys	Leu	Trp	Val	Tyr	Ile			
			340					345					350				

sequence listing_ST25.txt

<210> 167
<211> 912
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 + STR-tag (serotype d) sequence

<400> 167
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cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag 240
aacacaacat caggattcct aggaccctg ctcgtgttac aggcgggggtt tttcttggtg 300
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta 360
gggggagcac ccacgtgtcc tggccaaaat tcgcagtcac caacctccaa tcactcacca 420
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata 480
ttcctcttca tcctgctgct atgcctcatc ttcttggttg ttcttctgga ctaccaaggt 540
atgttgcccg tttgtcctct acttcagga acatcaacca ccagcacggg gccatgcaag 600
acctgcacga ttcctgctca aggaacctct atgtttccct cttgttgctg tacaaaacct 660
tcggacggaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta 720
tgggagtggg cctcagtcg tttctcctgg ctcagtttac tagtgccatt tgttcagtgg 780
ttcgtagggc tttccccac tgtttggtt tcagttatat ggatgatgtg gtattggggg 840
ccaagtctgt acaacatctt gagtcccttt ttacctctat taccaatttt cttttgtctt 900
tgggtatata tt 912

<210> 168
<211> 304
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 61-164 + STR-tag (serotype d) sequence

<400> 168

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

sequence listing_ST25.txt

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Trp
 50 55 60
 Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu
 65 70 75 80
 Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
 85 90 95
 Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
 100 105 110
 Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
 115 120 125
 Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
 130 135 140
 Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
 145 150 155 160
 Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
 165 170 175
 Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
 180 185 190
 Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
 195 200 205
 Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
 210 215 220
 Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
 225 230 235 240
 Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
 245 250 255
 Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val
 260 265 270
 Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
 275 280 285
 Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
 290 295 300

sequence listing_ST25.txt

<210> 169
<211> 912
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 (Q129R) + STR-tag (serotype d) sequence

<400> 169
atgggaggtt ggtcttccaa acctcgga aa ggcattggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag 240
aacacaacat caggattcct aggaccctg ctcgtgttac aggcggggtt tttcttgttg 300
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta 360
gggggagcac ccacgtgtcc tggccaaaat tcgcagtccc caacctccaa tcaactacca 420
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata 480
ttcctcttca tcctgctgct atgcctcatc ttcttgttgg ttcttctgga ctaccaaggt 540
atgttgcccg tttgtcctct acttccagga acatcaacca ccagcacggg gccatgcaag 600
acctgcacga ttctgctcg aggaacctct atgtttccct cttgttgctg tacaaaacct 660
tcggacggaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta 720
tgggagtggg cctcagtccg tttctcctgg ctcagtttac tagtgccatt tgttcagtgg 780
ttcgtagggc tttcccccac tgtttggtt tcagttatat ggatgatgtg gtattggggg 840
ccaagtctgt acaacatctt gagtcccttt ttacctctat taccaatttt cttttgtctt 900
tggtataca tt 912

<210> 170
<211> 304
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 61-164 (Q129R) + STR-tag (serotype d) sequence

<400> 170

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

sequence_listing_ST25.txt

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Trp
50 55 60

Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu
65 70 75 80

Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
85 90 95

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
100 105 110

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
115 120 125

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
130 135 140

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
145 150 155 160

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
165 170 175

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
180 185 190

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly
195 200 205

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
210 215 220

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
225 230 235 240

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
245 250 255

Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val
260 265 270

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
275 280 285

sequence listing_ST25.txt

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
290 295 300

<210> 171
<211> 912
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 (G145R) + STR-tag (serotype d) sequence

<400> 171
atgggaggtt ggtcttccaa acctcggaaa ggcattggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag 240
aacacaacat caggattcct aggacccttg ctcgtgttac aggcgggggtt tttcttggtg 300
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta 360
gggggagcac ccacgtgtcc tggccaaaat tcgcagtcac caacctccaa tctctacca 420
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata 480
ttcctcttca tcctgctgct atgcctcatc ttcttggttg ttcttctgga ctaccaaggt 540
atgttgcccg tttgtcctct acttcagga acatcaacca ccagcacggg gccatgcaag 600
acctgcacga ttcctgctca aggaacctct atgtttccct cttgttgctg tacaaaacct 660
tcggacagaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta 720
tgggagtggt cctcagtcg tttctcctgg ctcagtttac tagtgccatt tgttcagtgg 780
ttcgtagggc tttccccac tgtttggctt tcagttatat ggatgatgtg gtattggggg 840
ccaagtctgt acaacatctt gaggcccttt ttacctctat taccaatttt cttttgtctt 900
tgggtataca tt 912

<210> 172
<211> 304
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 61-164 (G145R) + STR-tag (serotype d) sequence

<400> 172

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
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sequence listing_ST25.txt

20

25

30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Trp
50 55 60

Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu
65 70 75 80

Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
85 90 95

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
100 105 110

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
115 120 125

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
130 135 140

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
145 150 155 160

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
165 170 175

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
180 185 190

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
195 200 205

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn
210 215 220

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
225 230 235 240

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
245 250 255

Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val
260 265 270

sequence listing_ST25.txt

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
275 280 285

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
290 295 300

<210> 173
<211> 912
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 (Q129R/G145R) + STR-tag (serotype d) sequence

<400> 173
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cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag 240
aacacaacat caggattcct aggaccctg ctcgtgttac aggcggggtt tttcttggtg 300
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta 360
gggggagcac ccacgtgtcc tggccaaaat tcgcagtccc caacctcaa tcactcacca 420
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata 480
ttcctcttca tcctgctgct atgcctcatc ttcttggttg ttcttctgga ctaccaaggt 540
atgttgcccg tttgtcctct acttccagga acatcaacca ccagcacggg gccatgcaag 600
acctgcacga ttctgctcg aggaacctct atgtttccct cttggttgctg tacaaaacct 660
tcggacagaa actgcacttg tattcccatc ccattcatcct gggctttcgc aagattccta 720
tgggagtggt cctcagtcctg tttctcctgg ctcagtttac tagtgccatt tgttcagtgg 780
ttcgtagggc tttccccac tgtttggctt tcagttatat ggatgatgtg gtattggggg 840
ccaagtctgt acaacatctt gagtcccttt ttacctctat taccaatttt cttttgtctt 900
tgggtataca tt 912

<210> 174
<211> 304
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 61-164 (Q129R/G145R) + STR-tag
(serotype d) sequence

<400> 174

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

sequence listing_ST25.txt

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Trp
50 55 60

Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu
65 70 75 80

Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
85 90 95

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
100 105 110

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
115 120 125

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
130 135 140

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
145 150 155 160

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
165 170 175

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
180 185 190

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly
195 200 205

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn
210 215 220

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
225 230 235 240

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
245 250 255

Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val
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sequence listing_ST25.txt

260

265

270

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
275 280 285

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
290 295 300

<210> 175
<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-1

<400> 175

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atggcctcgt accccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcccggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcggta ccttatgggc      540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc      600
accaacatcg tgcttggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct ggacctggct atgctggctg cgattcgccg cgtttacggg      720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggactgggga      780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc      840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgaggtt gctggccccc      900
aacggcgacc tgtataacgt gtttgccctg gccttggacg tcttgcccaa acgcctccgt      960
tccatgcacg tctttatcct ggattacgac caatcgcccc ccggctgccg ggacgccctg     1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggtctc cataccgacg     1080
atatgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                       1128
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<210> 176
<211> 1128

<212> PRT

<213> artificial sequence

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-2

<400> 176

Ala Thr Gly Gly Cys Thr Thr Cys Gly Thr Ala Cys Cys Cys Cys Thr
1 5 10 15

Gly Cys Cys Ala Thr Cys Ala Ala Cys Ala Cys Gly Cys Gly Thr Cys
20 25 30

Thr Gly Cys Gly Thr Thr Cys Gly Ala Cys Cys Ala Gly Gly Cys Thr
35 40 45

Gly Cys Gly Cys Gly Thr Thr Cys Thr Cys Gly Cys Gly Gly Cys Cys
50 55 60

Ala Thr Ala Gly Cys Ala Ala Cys Cys Gly Ala Cys Gly Thr Ala Cys
65 70 75 80

Gly Gly Cys Gly Thr Thr Gly Cys Gly Cys Cys Cys Thr Cys Gly Cys
85 90 95

cys Gly Gly Cys Ala Gly Cys Ala Ala Gly Ala Ala Gly Cys Cys Ala
100 105 110

cys Gly Gly Ala Ala Gly Thr Cys Cys Gly Cys Cys Thr Gly Gly Ala
115 120 125

Gly Cys Ala Gly Ala Ala Ala Ala Thr Gly Cys Cys Cys Ala Cys Gly
130 135 140

Cys Thr Ala Cys Thr Gly Cys Gly Gly Gly Thr Thr Thr Ala Thr Ala
145 150 155 160

Thr Ala Gly Ala Cys Gly Gly Thr Cys Cys Thr Cys Ala Cys Gly Gly
165 170 175

Gly Ala Thr Gly Gly Gly Gly Ala Ala Ala Ala Cys Cys Ala Cys Cys
180 185 190

Ala Cys Cys Ala Cys Gly Cys Ala Ala Cys Thr Gly Cys Thr Gly Gly
195 200 205

Thr Gly Gly Cys Cys Cys Thr Gly Gly Gly Thr Thr Cys Gly Cys Gly
210 215 220

Cys Gly Ala Cys Gly Ala Thr Ala Thr Cys Gly Thr Cys Thr Ala Cys
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sequence listing_ST25.txt															
225				230				235				240			
Gly	Thr	Ala	Cys	Cys ₂₄₅	Cys	Gly	Ala	Gly	Cys ₂₅₀	Cys	Gly	Ala	Thr	Gly ₂₅₅	Ala
Cys	Thr	Thr	Ala ₂₆₀	Cys	Thr	Gly	Gly	Cys ₂₆₅	Ala	Gly	Gly	Thr	Gly ₂₇₀	Cys	Thr
Gly	Gly	Gly ₂₇₅	Gly	Gly	Cys	Thr	Thr ₂₈₀	Cys	Cys	Gly	Ala	Gly ₂₈₅	Ala	Cys	Ala
Ala	Thr ₂₉₀	Cys	Gly	Cys	Gly	Ala ₂₉₅	Ala	Cys	Ala	Thr	Cys ₃₀₀	Thr	Ala	Cys	Ala
Cys ₃₀₅	Cys	Ala	Cys	Ala	Cys ₃₁₀	Ala	Ala	Cys	Ala	Cys ₃₁₅	Cys	Gly	Cys	Cys	Thr ₃₂₀
Cys	Gly	Ala	Cys	Cys ₃₂₅	Ala	Gly	Gly	Gly	Thr ₃₃₀	Gly	Ala	Gly	Ala	Thr ₃₃₅	Ala
Thr	Cys	Gly	Gly ₃₄₀	Cys	Cys	Gly	Gly	Gly ₃₄₅	Gly	Ala	Cys	Gly	Cys ₃₅₀	Gly	Gly
Cys	Gly	Gly ₃₅₅	Thr	Gly	Gly	Thr	Ala ₃₆₀	Ala	Thr	Gly	Ala	Cys ₃₆₅	Ala	Ala	Gly
Cys	Gly ₃₇₀	Cys	Cys	Cys	Ala	Gly ₃₇₅	Ala	Thr	Ala	Ala	Cys ₃₈₀	Ala	Ala	Thr	Gly
Gly ₃₈₅	Gly	Cys	Ala	Thr	Gly ₃₉₀	Cys	Cys	Thr	Thr	Ala ₃₉₅	Thr	Gly	Cys	Cys	Gly ₄₀₀
Thr	Gly	Ala	Cys	Cys ₄₀₅	Gly	Ala	Cys	Gly	Cys ₄₁₀	Cys	Gly	Thr	Thr	Cys ₄₁₅	Thr
Gly	Gly	Cys	Thr ₄₂₀	Cys	Cys	Thr	Cys	Ala ₄₂₅	Thr	Gly	Thr	Cys	Gly ₄₃₀	Gly	Gly
Gly	Gly	Gly ₄₃₅	Gly	Ala	Gly	Gly	Cys ₄₄₀	Thr	Gly	Gly	Gly	Ala ₄₄₅	Gly	Thr	Thr
Cys	Ala ₄₅₀	Cys	Ala	Thr	Gly	Cys ₄₅₅	Cys	Cys	Cys	Gly	Cys ₄₆₀	Cys	Cys	Cys	Cys
Gly ₄₆₅	Gly	Cys	Cys	Cys	Thr ₄₇₀	Cys	Ala	Cys	Cys	Cys ₄₇₅	Thr	Cys	Ala	Thr	Cys ₄₈₀

sequence_listing_ST25.txt

Thr Thr Cys Gly Ala Cys Cys Gly Cys Cys Ala Thr Cys Cys Cys Ala
485 490 495

Thr Cys Gly Cys Cys Gly Cys Cys Cys Thr Cys Cys Thr Gly Thr Gly
500 505 510

Cys Thr Ala Cys Cys Cys Gly Gly Cys Cys Gly Cys Gly Cys Gly Ala
515 520 525

Thr Ala Cys Cys Thr Thr Ala Thr Gly Gly Gly Cys Ala Gly Cys Ala
530 535 540

Thr Gly Ala Cys Cys Cys Cys Cys Cys Ala Gly Gly Cys Cys Gly Thr
545 550 555 560

Gly Cys Thr Gly Gly Cys Gly Thr Thr Cys Gly Thr Gly Gly Cys Cys
565 570 575

Cys Thr Cys Ala Thr Cys Cys Cys Gly Cys Cys Gly Ala Cys Cys Thr
580 585 590

Thr Gly Cys Cys Cys Gly Gly Cys Ala Cys Ala Ala Ala Cys Ala Thr
595 600 605

Cys Gly Thr Gly Thr Thr Gly Gly Gly Gly Gly Cys Cys Cys Thr Thr
610 615 620

Cys Cys Gly Gly Ala Gly Gly Ala Cys Ala Gly Ala Cys Ala Cys Ala
625 630 635 640

Thr Cys Gly Ala Cys Cys Gly Cys Cys Thr Gly Gly Cys Cys Ala Ala
645 650 655

Ala Cys Gly Cys Cys Ala Gly Cys Gly Cys Cys Cys Cys Gly Gly Cys
660 665 670

Gly Ala Gly Cys Gly Gly Cys Thr Thr Gly Ala Cys Cys Thr Gly Gly
675 680 685

Cys Thr Ala Thr Gly Cys Thr Gly Gly Cys Cys Gly Cys Gly Ala Thr
690 695 700

Thr Cys Gly Cys Cys Gly Cys Gly Thr Thr Thr Ala Cys Gly Gly Gly
705 710 715 720

Cys Thr Gly Cys Thr Thr Gly Cys Cys Ala Ala Thr Ala Cys Gly Gly
725 730 735

sequence listing_ST25.txt

Thr Gly Cys Gly Gly Thr Ala Thr Cys Thr Gly Cys Ala Gly Gly Gly
740 745 750

Cys Gly Gly Cys Gly Gly Gly Thr Cys Gly Thr Gly Gly Thr Gly Gly
755 760 765

Gly Ala Gly Gly Ala Thr Thr Gly Gly Gly Gly Ala Cys Ala Gly Cys
770 775 780

Thr Thr Thr Cys Gly Gly Gly Gly Ala Cys Gly Gly Cys Cys Gly Thr
785 790 795 800

Gly Cys Cys Gly Cys Cys Cys Cys Ala Gly Gly Gly Thr Gly Cys Cys
805 810 815

Gly Ala Gly Cys Cys Cys Cys Ala Gly Ala Gly Cys Ala Ala Cys Gly
820 825 830

Cys Gly Gly Gly Cys Cys Cys Ala Cys Gly Ala Cys Cys Cys Cys Ala
835 840 845

Thr Ala Thr Cys Gly Gly Gly Gly Ala Cys Ala Cys Gly Thr Thr Ala
850 855 860

Thr Thr Thr Ala Cys Cys Cys Thr Gly Thr Thr Thr Cys Gly Gly Gly
865 870 875 880

Cys Cys Cys Cys Cys Gly Ala Gly Thr Thr Gly Cys Thr Gly Gly Cys
885 890 895

Cys Cys Cys Cys Ala Ala Cys Gly Gly Cys Gly Ala Cys Cys Thr Gly
900 905 910

Thr Ala Thr Ala Ala Cys Gly Thr Gly Thr Thr Thr Gly Cys Cys Thr
915 920 925

Gly Gly Gly Cys Cys Thr Thr Gly Gly Ala Cys Gly Thr Cys Thr Thr
930 935 940

Gly Gly Cys Cys Ala Ala Ala Cys Gly Cys Cys Thr Cys Cys Gly Thr
945 950 955 960

Cys Cys Cys Ala Thr Gly Cys Ala Cys Gly Thr Cys Thr Thr Thr Ala
965 970 975

Thr Cys Cys Thr Gly Gly Ala Thr Thr Ala Cys Gly Ala Cys Cys Ala
980 985 990

sequence listing_ST25.txt

Ala Thr Cys Gly Cys Cys Cys Gly Cys Cys Gly Gly Cys Thr Gly Cys
995 1000 1005

Cys Gly Gly Gly Ala Cys Gly Cys Cys Cys Thr Gly Cys Thr Gly
1010 1015 1020

Cys Ala Ala Cys Thr Thr Ala Cys Cys Thr Cys Cys Gly Gly Gly
1025 1030 1035

Ala Thr Gly Gly Thr Cys Cys Ala Gly Ala Cys Cys Cys Ala Cys
1040 1045 1050

Gly Thr Cys Ala Cys Cys Ala Cys Cys Cys Cys Ala Gly Gly Cys
1055 1060 1065

Thr Cys Cys Ala Thr Ala Cys Cys Gly Ala Cys Gly Ala Thr Cys
1070 1075 1080

Thr Gly Cys Gly Ala Cys Cys Thr Gly Gly Cys Gly Cys Gly Cys
1085 1090 1095

Ala Cys Gly Thr Thr Thr Gly Cys Cys Cys Gly Gly Gly Ala Gly
1100 1105 1110

Ala Thr Gly Gly Gly Gly Gly Ala Gly Gly Cys Thr Ala Ala Cys
1115 1120 1125

<210> 177
<211> 1128
<212> DNA
<213> artificial sequence

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-3

<400> 177
atggcttcgt accccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttcgcg cctcgccggc agcaagaagc cacggaagtc 120
cgccccgagc agaaaatgcc cagcgtactg cggggtttata tagacgggtcc ccacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccgggggacgc ggcgggtggtg 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc 480

sequence listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcggtg ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
accaacatcg tgcttggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct ggacctggct atgctggctg cgattcgccg cgtttacggg	720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggg cgtggcgggg ggactgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtataacgt gtttgccctg gccttggacg tcttgccaa acgcctccgt	960
tccatgcacg tctttatcct ggattacgac caatcgcccc ccggctgccg ggacgcctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggtc cataccgacg	1080
atatgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 178

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-4

<400> 178

atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgatc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tggtgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggg cgtggcgggg ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtataacgt gtttgccctg gccttggacg tcttgccaa acgcctccgt	960

sequence listing_ST25.txt

```

cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcgccg gagatggggg aggctaac 1128

```

```

<210> 179
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-5

```

```

<400> 179
atggcttcgt accccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgaccggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcgggtg ttcggggctt ccgagacaat cgcgaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ctttatgggc 540
agcatgaccc cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggtt tgacctggt atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccaca tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgcttg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcgccg gagatggggg aggctaac 1128

```

```

<210> 180
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-6

```


sequence listing_ST25.txt

```

<400> 180
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccgccctt caccctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ccttatgggc      540
agcatgacct cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc      600
acaaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg      720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga      780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca      840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggccccc      900
aacggcgacc tgtataacgt gtttgcttgg gccttggacg tcttgccaa acgcctccgt      960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg     1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                    1128

```

```

<210> 181
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-7

```

```

<400> 181
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct      420

```

sequence listing_ST25.txt

cctcatatcg	ggggggagggc	tgggagctca	catgccccgc	ccccggccct	caccctcatc	480
ttcgaccgcc	atcccatcgc	cgccctcctg	tgctaccggg	ccgcgcgata	ccttatgggc	540
agcatgaccc	cccaggccgt	gctggcgttc	gtggccctca	tcccgccgac	cttgcccggc	600
acaaacatcg	tgttgggggc	ccttccggag	gacagacaca	tcgaccgcct	ggccaaacgc	660
cagcgccccg	gcgagcggct	tgacctggct	atgctggccg	cgattcgccg	cgtttacggg	720
ctgcttgcca	atacggtgcg	gtatctgcag	ggcggcgggg	cgtggcggga	ggattgggga	780
cagctttcgg	ggacggccgt	gccgccccag	ggtgccgagc	cccagagcaa	cgcgggccca	840
cgaccccata	tcggggacac	gttatttacc	ctgtttcggg	cccccgagtt	gctggccccc	900
aacggcgacc	tgtataacgt	gtttgcctgg	gccttgagcg	tcttgccaa	acgcctccgt	960
cccatgcacg	tctttatcct	ggattacgac	caatcgcccc	ccggctgccg	ggacgcccctg	1020
ctgcaactta	cctccgggat	ggtccagacc	cacgtcacca	ccccaggctc	cataccgacg	1080
atctgcgacc	tggcgcgcac	gtttgcccgg	gagatggggg	aggctaac		1128

<210> 182

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-8

<400> 182

atggcttcgt	acccttgcca	tcaacacgcg	tctgcgttcg	accaggctgc	gcgttctcgc	60
ggccatagca	accgacgtac	ggcgttgcg	cctcgccggc	agcaagaagc	cacggaagtc	120
cgcctggagc	agaaaatgcc	cacgctactg	cgggtttata	tagacggtcc	tcacgggatg	180
gggaaaacca	ccaccacgca	actgctggtg	gccctgggtt	cgcgcgacga	tatcgtctac	240
gtacccgagc	cgatgactta	ctggcagggtg	ctgggggctt	ccgagacaat	cgcgaaacatc	300
tacaccacac	aacaccgcct	cgaccagggt	gagatatcgg	ccggggatgc	ggcggtggtgta	360
atgacaagcg	cccagataac	aatgggcatg	ccttatgccg	tgaccgacgc	cgttctggct	420
cctcatatcg	ggggggagggc	tgggagctca	catgccccgc	ccccggccct	caccctcatc	480
ttcgaccgcc	atcccatcgc	cgccctcctg	tgctaccggg	ccgcgcgata	ccttatgggc	540
agcatgaccc	cccaggccgt	gctggcgttc	gtggccctca	tcccgccgac	cttgcccggc	600
acaaacatcg	tgttgggggc	ccttccggag	gacagacaca	tcgaccgcct	ggccaaacgc	660
cagcgccccg	gcgagcggct	tgacctggct	atgctggccg	cgattcgccg	cgtttacggg	720
ctgcttgcca	atacggtgcg	gtatctgcag	ggcggcgggg	cgtggcggga	ggattgggga	780
cagctttcgg	ggacggccgt	gccgccccag	ggtgccgagc	cccagagcaa	cgcgggccca	840

sequence listing_ST25.txt

```

cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttggacg tcttggccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggtc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

```

```

<210> 183
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-9

```

```

<400> 183
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccataaca accgacgtac ggcgttcgc cctcgccggc agcaagaagc cacggaagtc 120
cgctggagc agaaaatgcc cacgtactg cgggtttata tagacgtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcg cgggggatgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg taaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc cccggccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ccttatgggc 540
agcatgaccc cccaggccgt gctggcgctt ttggccctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggg cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttggacg tcttggccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggtc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

```

```

<210> 184
<211> 1128
<212> DNA
<213> artificial sequence

```

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-10

<400> 184

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atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc      120
cacctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcagggt ctgggggctt ccgagacaat cggaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggy ccgcgcgata ccttatgggc      540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc      600
acaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg      720
ctgcttgcca atacggtgcg gtatctgcag ggcggcggggt cgtggcgggg ggattgggga      780
cagctttcgg ggacggccgt gccacccag ggtgccgagc cccagagcaa cgcgggccca      840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagatt gctggccccc      900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccag acgcctccgt      960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg     1020
ctgcaactta cctccgggat ggtccagacc cacgtacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                    1128

```

<210> 185

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-11

<400> 185

```

atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc      120
cgcttgagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240

```

sequence listing_ST25.txt

gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccgggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttccagag gacaaacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgtca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 186
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-12

<400> 186	
atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccgggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttccggag gacagacaca tcgaccgcct ggccaaacgc	660

sequence listing_ST25.txt

cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgga ggattggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggcacc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgac gttgcccgg gagatggggg aggctaac	1128

<210> 187
 <211> 1128
 <212> DNA
 <213> artificial sequence
 <220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-13

<400> 187

atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cgccctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggt	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ccttatgggc	540
agcatgacc cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc cttccggag gacagacaca ttgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctagccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgga ggattggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080

sequence_listing_ST25.txt

atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 188
<211> 1128
<212> DNA
<213> artificial sequence

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-14

<400> 188
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg 360
atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ctttatgggc 540
agcatgacct cccaggccgt gctggcggtt gtggccctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc ctttcggag gagagacaca ttgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgggg ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgggcaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 189
<211> 1128
<212> DNA
<213> artificial sequence

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-15

<400> 189
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60

sequence listing_ST25.txt

```

ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccaggtt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctt tgctaccggc ccgcgcgata ccttatgggc 540
agcatgaccc cccaggccgt gctggcggtt gtggccctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc ccttccggag gacagacaca ttgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggccccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

```

```

<210> 190
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-16

```

```

<400> 190
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ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccaggtt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480

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sequence listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgctaccg	ccgcgcgata ctttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca	tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc cttccggag gacagacaca	tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctagccg	cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt	cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc	cccagagcaa cgcgggccca	840
cgacccccata tcggggacac gttatttacc ctgtttcggg	ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgacg	tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg	ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca	cccaggctc cataccgacg	1080
atctgcgacc tggcgcgac gttgcccgg gagatggggg	aggctaac	1128

<210> 191
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-17

<400> 191	
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ggccatagca accgacgtac ggcgttgcg cctcgccggc	agcaagaagc cacggaagtc 120
cgcttgagc agaaaatgcc cacgctactg cgggtttata	tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctggggt	cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt	ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccaggtg gagatatcg	ccggggacgc ggcggtggtg 360
atgacaagcg cccagataac aatgggcatg ctttatgccg	tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc	ccccggccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccg	ccgcgcgata ctttatgggc 540
agcatgaccc cccaggccgt gctggcggtc gtggccctca	tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc cttccggag gacagacaca	tcgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctagccg	cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt	cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc	cccagagcaa cgcggaacca 840
cgacccccata tcggggacac gttatttacc ctgtttcggg	ccccgagtt gctggcccc 900

sequence listing_ST25.txt

aacggcgacc tgtataacgt gtttgccctgg gccttgagacg tcttgcccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgccccg gagatggggg aggctaac	1128

<210> 192
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-18

<400> 192	
atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgtactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccaggtt gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccgccctt caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ccttatgggc	540
agcatgacct cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctagccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggc cgtggcgggg ggattgggga	780
cagctttcgg ggacggccgt gccgccccag gttgccgagc cccagagcaa cgcggaccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagttt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctgg gccttgagacg tcttgcccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgccccg gagatggggg aggctaac	1128

<210> 193
 <211> 1128
 <212> DNA
 <213> artificial sequence

sequence_listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-19

<400> 193

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atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
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cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcagggt ctgggggctt ccgagacaat cgcgaaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct catcctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ccttatgggc      540
agcatgacct cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc      600
acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctagccg cgattcgccg cgtttacggg      720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggc cgtggcgggg ggattgggga      780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca      840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagatt gctggcccccc      900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgggcaa acgcctccgt      960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg     1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                     1128
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<210> 194

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-20

<400> 194

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atggcttcgt atccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
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sequence listing_ST25.txt

gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccaccc aacaccgcct cgaccagggg gagatatcgg ccgggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
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cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgaccccata tcgggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgcacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 195

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-21

<400> 195

atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccgggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc	660

```

sequence_listing_ST25.txt
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
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cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgcttg gccttgagc tcttggtcaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgccc cggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

```

```

<210> 196
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-22

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```

<400> 196
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cagctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggta ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc 540
agcatgaccc cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcggggt cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
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aacggcgacc tgtataacgt gtttgcttg gccttgagc tcttggtcaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgccc cggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080

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sequence listing_ST25.txt

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<210> 197
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-23

<400> 197
 atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
 ggccatagca accgacgtac ggcggtgcgc cctcgccggc agcaagaagc cacggaagtc 120
 cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
 gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
 gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
 tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg 360
 atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
 cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
 ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ctttatgggc 540
 agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc 600
 acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc 660
 cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
 ctgcttgcca atacggtgcg gtatctgcag ggcggcgggc cgtggcgggg ggattggggg 780
 cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
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 cccatgcacg tctttatcct ggattacgac caagcgcccg ccggctgccg ggacgccctg 1020
 ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
 atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 198
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-24

<400> 198
 atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgt 60

sequence listing_ST25.txt

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ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacgggcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg cttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc cccggccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata cttatgggc 540
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cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
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cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
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aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
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atctgcgacc tggcgcgcac gttgccccg gagatggggg aggctaac 1128

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<210> 199

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-25

<400> 199

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ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacgggcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg cttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc cccggccct caccctcatc 480

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sequence listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggg cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccaca tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggccccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggtgccc ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 200
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-26

<400> 200	
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ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcttgagc agaaaatgcc cagcgtactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcggggt ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct cgccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggg cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggccccc	900

sequence listing_ST25.txt

aacggcgacc tgtacaacgt gtttgcctgg gccttggacg tcttggccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat gatccagacc cacgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 201
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-27

<400> 201	
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ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cggccggagc agaaaatgcc cacgctactg cgggtttata tagacgggtc ccacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg ccagataaac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ccttatgggc	540
agcatgacct ccagggcgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggt tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc ccagagcaa cgcgggcca	840
cgacccaca tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgcctgg gccttggacg tcttggccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 202
 <211> 1128
 <212> DNA
 <213> artificial sequence

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-28

<400> 202

```

atggcttcgt accccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcccgagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg cccagataac aatgggcatg cttatgccc tgaccgacgc cgttctggct      420
cctcatatcg ggggggagc tgggagctca catgccccgc cccggccct caccctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata cttatgggc      540
agcatgaccc cccaggccgt gttggcggtc gtggccctca tccgcccac cttgcccggc      600
acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg      720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga      780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca      840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccagatt gctggcccc      900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt      960
cccatgcacg tctttatcct ggattacgac caatcgccc cggtctgccg ggacgccctg     1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                    1128

```

<210> 203

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-29

<400> 203

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atggcttcgt accccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcccgagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240

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sequence listing_ST25.txt

gtacccgagc cgatgactta ctggcggggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggg ccgcgcgata ccttatgggc	540
agcatgacct cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgacccccaca tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 204

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-30

<400> 204

atggcttcgt acccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcccggagc agaaaatgcc cacgctactg cgggtttata tagacggccc ccacgggatg	180
gggaaaacca ccaccacgca actgctgggt gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcggggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggg ccgcgcgata ccttatgggc	540
agcatgacct cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc	660

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sequence_listing_ST25.txt
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccaca tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggccccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaac 1128

```

```

<210> 205
<211> 1128
<212> DNA
<213> artificial sequence

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<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-31

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<400> 205
atggcttcgt acccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcccgagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccg cgcgcgata ccttatgggc 540
agcatgaccc cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc 600
acaaacatcg tggtgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag gccggcgggt cgtggcggca ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccaca tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggccccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaaggctc cataccgacg 1080

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sequence_listing_ST25.txt

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<210> 206
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-32

<400> 206
 atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
 ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
 cgcttgagc agaaaatgcc cacgctactg cgggtttata tagacgggcc tcacgggatg 180
 gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
 gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cggaacatc 300
 tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggtg 360
 atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
 cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
 ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ctttatgggc 540
 agcatgacct cccaggccgt gctggcgttc gtggccctca tcccgccgac cttggccggc 600
 acaaacatcg tggtgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc 660
 cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
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 cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
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 aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
 cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg 1020
 ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
 atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 207
 <211> 1131
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-33

<400> 207
 atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60

sequence listing_ST25.txt

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cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccg cgcgcgata ccttatgggc	540
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acaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgcgccg gcgagcggt tgacctggt atgctggccg cgattcgccg cgtttacggg	720
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<210> 208
 <211> 1131
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-34

<400> 208	
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cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480

sequence listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
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caaacatcgt gttggggggc cttccggagg acagacacat cgaccgcctg gccaaacgcc	660
agcgccccgg cgagcggctt gacctggcta tgctggccgc gattcgccgc gtttacgggc	720
tgcttgccaa tacggtgcgg tatctgcagg gcggcgggtc gtggcgggag gattggggac	780
agctttcggg gacggccgtg ccgccccagg gtgccgagcc ccagagcaac gcgggcccac	840
gaccccatat cggggacacg ttattttacc tgtttcgggc ccccgagttg ctggccccca	900
acggcgacct gtataacgtg tttgcctggg ccttgacgt cttggccaaa cgcctccgtc	960
ccatgcacgt ctttatcctg gattacgacc aatcgccgc cggtgcccgg gacgccctgc	1020
tgcaacttac ctccgggatg gtccagaccc acgtcaccac cccaggctcc ataccgacga	1080
tctgcgacct ggcgcgcacg tttggccggg agatggggga ggctaactga a	1131

<210> 209

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-35

<400> 209

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ggccatagca accgacgtac ggcgttcgc cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata taaacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg cgggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc	660
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cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900

sequence listing_ST25.txt

aacggcgacc	tgtataacgt	gtttgcctgg	gccttggacg	tcttggccaa	acgcctccgt	960
cccatgcacg	tctttatcct	ggattacgac	caatcgcccc	ccggctgccg	ggacgccctg	1020
ctgcaactta	cctccgggat	ggtccagacc	cacgtcacca	ccccaggctc	cataccgacg	1080
atctgcgacc	tggcgcgcac	gtttgcccgg	gagatggggg	aggctaac		1128

<210> 210
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-36

<400>	210	
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atggcttcgt	acccctgcc	
tcaacacg	tctgcgttcg	120
accaggtgc	gcgttctcgc	
ggccatagca	accgacgtac	180
ggcgttg	cctcgccggc	
agcaagaagc	cacggaagtc	240
cgctggagc	agaaaatgcc	
cacgctactg	cggtttata	300
tagacggtcc	tcacgggatg	
gggaaaacca	ccaacacgca	360
actgctggtg	gccctgggtt	
cgcgcgacga	tatcgtctac	420
gtacccgagc	cgatgactta	
ctggcaggtg	ctgggggctt	480
ccgagacaat	cgcgaaacatc	
tacaccacac	aacaccgcct	540
cgaccagggt	gagatatcgg	
ccggggacgc	ggcgggtggt	600
atgacaagcg	cccagataac	
aatgggcatg	ccttatgccg	660
tgaccgacgc	cgttctggct	
cctcatatcg	ggggggaggc	720
tgggagctca	catgccccgc	
ccccggccct	caccctcatc	780
tctgaccgcc	atcccatcgc	
cgccctcctg	tgctaccgg	840
ccgcgcgata	ccttatgggc	
agcatgaccc	cccaggccgt	900
gctggcgctt	gtggccctca	
tcccgccgac	cttgcccggc	960
acaaacatcg	tggtgggggc	
ccttccggag	gacagacaca	1020
tcgaccgcct	ggccaaacgc	
cagcgccccg	gcgagcggct	1080
tgacctggct	atgctggccg	
cgattcgccg	cgtttacggg	1128
ctgcttgcca	atacgggtgcg	
gtatctgcag	ggcggcgggg	
cgtggcgggg	ggattggggg	
cagctttcgg	ggacggccgt	
gccgccccag	ggtgccgagc	
cccagagcaa	cgcgggccca	
cgaccccata	tcggggacac	
gttatttacc	ctgtttcggg	
cccccgagtt	gctggccccc	
aacggcgacc	tgtataacgt	
gtttgcctgg	gccttggacg	
tcttggccaa	acgcctccgt	
cccatgcacg	tctttatcct	
ggattacgac	caatcgcccc	
ccggctgccg	ggacgccctg	
ctgcaactta	cctccgggat	
ggtccagacc	cacgtcacca	
ccccaggctc	cataccgacg	
atctgcgacc	tggcgcgcac	
gtttgcccgg	gagatggggg	
aggctaac		

<210> 211
 <211> 1128
 <212> DNA
 <213> artificial sequence

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-37

<400> 211

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atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagt cgatgactta ctggcagggt ctgggggctt ccgagacaat cggaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggc tgggagctca catgccccgc cccgggccct caccctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ccttatgggc      540
agcatgacc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc      600
acáaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg      720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga      780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca      840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccagagtt gctggccccc      900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttggccaa acgcctccgt      960
cccattgcac tctttatcct ggattacgac caatcgcccg ccggtgccc ggacgccctg     1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                    1128

```

<210> 212

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-38

<400> 212

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atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240

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sequence listing_ST25.txt

gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttcgggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgcttg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccc cggtcgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 213
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-39

<400> 213	
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ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgccctgc	600
acaaacatcg tgttgggggc ccttcgggag gacagacaca tcgaccgcct ggccaaacgc	660

sequence_listing_ST25.txt

cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgga ggattggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcca	840
cgacccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgac gtttgcccg gagatggggg aggctaac	1128

<210> 214
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-40

<400> 214	
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ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ccttatgggc	540
agcatgacct cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
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cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcca	840
cgacccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080

sequence listing_ST25.txt

atctgcgacc tggcgcgcac gtttggcccg gagatggggg aggctaac 1128

<210> 215
<211> 1128
<212> DNA
<213> artificial sequence

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-41

<400> 215
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ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cggaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc cccggccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ccttatgggc 540
agcatgacc cccaggccgt gctggcggtt gtggccctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
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cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccata tcggggacat gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgacg tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttggcccg gagatggggg aggctaac 1128

<210> 216
<211> 1128
<212> DNA
<213> artificial sequence

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-42

<400> 216
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sequence listing_ST25.txt

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ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
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gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcagggtg ctgggggctt ccgagacaat cgcgaacatc 300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ccttatgggc 540
agcatgaccc cccaggccgt gctggcggtt gtggccctca tcccgccgac cttgcccggc 600
acaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgcgccg gcgagcggtt tgacctggct atgctggccg cgattcgccg cgtttacggg 720
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cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctaccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggtc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaac 1128

```

```

<210> 217
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-43

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```

<400> 217
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cgcccggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc 300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480

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sequence listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ctttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tggtgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgggg ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
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ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgac gttgccccg gagatggggg aggctaac	1128

<210> 218
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-44

<400> 218	
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cgcttgagc agaaaatgcc cagctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cggaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcg cggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ctttatgggc	540
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cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggcccc	900

sequence listing_ST25.txt

aacggcgacc tgtataacgt gtttgcctgg gccttggacg tcttggccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccccggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg ggagtggggg aggctaac	1128

<210> 219
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-45

<400> 219	
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ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cggccggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
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atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccgccctt caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcggta ccttatgggc	540
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acaaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
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aacggcgacc tgtacaacgt gtttgcctgg gccttggacg tcttggccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctcac	1128

<210> 220
 <211> 1128
 <212> DNA
 <213> artificial sequence

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-46

<400> 220

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cgcctggagc agaaaatgcc cacgctactg tgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcagggt ctgggggctt ccgagacaat cgcgaaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg      360
atgacaagcg ccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggg ccgcgcgata ccttatgggc      540
agcatgaccc ccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc      600
acaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg      720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga      780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc ccagagcaa cgcgggccca      840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgaggtt gctggccccc      900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt      960
cccattgcag tctttatcct ggattacgac caatcgcccg ccggtgccg ggacgccctg     1020
ctgcaactta cctccgggat ggtccagacc cacgtacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                     1128
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<210> 221

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-47

<400> 221

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ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
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sequence listing_ST25.txt

gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcggtg ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tggtgggggc ccttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggcca	840
cgaccccata tcggggaaac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtacaacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggtgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg aggtcac	1128

<210> 222
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-48

<400> 222	
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ggccatagca accgacgtac ggcgttgccg cctcgccggc aacaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cagctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgttaccggc ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tggtgggggc ccttccggag gacagacaca tcgaccgcct ggccaaacgc	660

sequence listing_ST25.txt

cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacgag	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgcttg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccc cggtcgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggtc cataccgacg	1080
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<210> 223
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-49

<400> 223	
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cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgttaccgg ccgtgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tggtgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacgag	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgcttg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccc cggtcgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggtc cataccgacg	1080

sequence listing_ST25.txt

atctgcgacc cggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 224
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-50

<400> 224
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 ggccatagca accgacgtac ggcgttgccg cctcgccggc aacaagaagc cacggaagtc 120
 cgcttgagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
 gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
 gtacccgagc cgataactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
 tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg 360
 atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cggttctggct 420
 cctcatatcg ggggggaggc tgggagctca catgccccgc cccggccct caccctcatc 480
 ttcgaccggc atcccatcgc cgccctcctg tgttaccggc ccgcgcgata ccttatgggc 540
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 cagcgcgccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacgag 720
 ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
 cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
 cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
 aacggcgacc tgtataacgt gtttgccctg gccttgacg tcttgccaa acgcctccgt 960
 cccatgcacg tctttatcct ggattacgac caatcgccg ccggtgccg ggacgccctg 1020
 ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggtc cataccgacg 1080
 atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 225
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-51

<400> 225
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sequence listing_ST25.txt

ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggtcctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgaccccata tcggggaaac gttatttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtacaacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaac	1128

<210> 226
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-52

<400> 226	
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ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtaccaagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480

sequence listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggtcctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggattgggga	780
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cgaccccata tcggggaaac gttatttacc ctgtttcggg cccccgagtt gctggccccc	900
aacggcgacc tgtacaacgt gtttgccctg gccttgagc tcttgggcaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggtgcccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 227
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-53

<400> 227	
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ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cagcgtactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtaccaagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggtcctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
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cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggaaac gttatttacc ctgtttcggg cccccgagtt gctggccccc	900

sequence listing_ST25.txt

aacggcgacc tgtacaacgt gtttgccctgg gccttggacg tcttgcccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaac	1128

<210> 228
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-54

<400> 228	
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ggccatagca accgacgtac ggcgttgccg cctcgccggc aacaagaagc cacggaagtc	120
cgcccggagc agaaaatgcc cacgctactg cgggtttata tagacgggtc tcacgggatg	180
gggaaaacca ccaccacgca actgctgggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcggggt ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aaccccgct cgaccagggt gagatatcgg ccggggacgc ggcgggtggt	360
atgacaagcg ccagataaac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
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acaaacatcg tgcttggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggctg cgattcgccg cgtttacgag	720
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cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggaaac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtacaacgt gtttgccctgg gccttggacg tcttgcccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg cggctaac	1128

<210> 229
 <211> 1128
 <212> DNA
 <213> artificial sequence

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-55

<400> 229

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ggccatagca	accgacgtac	ggcgttgcg	cctcgccggc	aacaagaagc	cacggaagtc	120
cgcctggagc	agaaaatgcc	cacgctactg	cgggtttata	tagacggtcc	tcacgggatg	180
gggaaaacca	ccaccacgca	actgctggtg	gccctggggt	cgcgcgacga	tatcgtctac	240
gtacccgagc	cgatgactta	ctggcgggtg	ctgggggctt	ccgagacaat	cggaacatc	300
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acaaacatcg	tgcttggggc	ccttcgggag	gacagacaca	tcgaccgcct	ggccaaacgc	660
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ctacttgcca	atacggtgcg	gtatctgcag	tgcggcgggt	cgtggcgggg	ggactgggga	780
cagcttttcg	ggacggccgt	gacgccccag	ggtgccgagc	cccagagcaa	cgcgggccca	840
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aacggcgacc	tgtacaacgt	gtttgcctgg	gccttgagcg	tcttgcccaa	acgcctccgt	960
cccatgcacg	tctttatcct	ggattacgac	caatcgcccc	ccggctgccg	ggacgccctg	1020
ctgcaactta	cctccgggat	ggtccagacc	catgtcacca	ccccaggctc	cataccgacg	1080
atctgcgacc	tggcgcgcac	gtttgcccgg	gagatggggg	aggctcac		1128

<210> 230

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-56

<400> 230

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ggccatagca	accgacgtac	ggcgttgcg	cctcgccggc	agcaagaagc	cacggaagtc	120
cggccggagc	agaaaatgcc	cacgctactg	cgggtttata	tagacggtcc	ccacgggatg	180
gggaaaacca	ccaccacgca	actgctggtg	gccctggggt	cgcgcgacga	tatcgtctac	240

sequence_listing_ST25.txt

gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtt gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
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cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccaca tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgacg tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 231

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-57

<400> 231

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ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cacctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggg ccgcgcggta ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtt gtggtcctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc	660

sequence listing_ST25.txt

cagcgccccg	gtgagcggct	tgacctggct	atgctggccg	cgattcgccg	cgtttacggg	720
ctacttgcca	atacgggtgcg	gtatctgcag	tgcggcgggt	cgtaggcggga	ggattgggga	780
cagcttttcgg	ggacggcctt	gacgccccag	ggtgccgagc	cccagagcaa	cgcgggccca	840
cgaccccata	tcggggaaac	gttattttacc	ctgttttcggg	cccccgagtt	gctggccccc	900
aacggcgacc	tgtacaacgt	gtttgccttg	gccttgagc	tcttgccaa	acgcctccgt	960
cccatgcacg	tctttatcct	ggattacgac	caatcgcccg	ccggctgccg	ggacgccctg	1020
ctgcaactta	cctccgggat	ggtccagacc	cacgtcacca	ccccggctc	cataccgacg	1080
atctgcgacc	tggcgcgcac	gtttgcccgg	gagatggggg	aggctaac		1128

<210> 232

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-58

<400> 232

atggcttcgt	accccgcca	tcaacacgcg	tctgcgttcg	accaggctgc	gcgttctcgc	60
ggccatagca	accgacgtac	ggcgttgccg	cctcgccggc	agcaagaagc	cacggaagtc	120
cacctggagc	agaaaatgcc	cacgctactg	cgggtttata	tagacggtcc	tcacgggatg	180
gggaaaacca	ccaccacgca	actgctggtg	gccctggggt	cgcgcgacga	tatcgtctac	240
gtacccgagc	cgatgactta	ctggcggggtg	ctgggggctt	ccgagacaat	cgcgaaacatc	300
tacaccacac	aacaccgcct	cgaccagggt	gagatatcgg	ccggggacgc	ggcgggtggt	360
atgacaagcg	cccagataac	aatgggcatg	ccttatgccg	tgaccgacgc	cgttctggct	420
cctcatatcg	ggggggaggc	tgggagctca	catgccccgc	ccccggccct	caccctcatc	480
ttcgaccacc	atcccatcgc	cgccctcctg	tgctaccccg	ccgcgcggta	ccttatgggc	540
agcatgaccc	cccaggccgt	gctggcggtc	gtggtcctca	tcccgccgac	cttgcccggc	600
acaaacatcg	tgttgggggc	ccttcgggag	gacagacaca	tcgaccgcct	ggccaaacgc	660
cagcgccccg	gtgagcggct	tgacctggct	atgctggccg	cgattcgccg	cgtttacggg	720
ctacttgcca	atacgggtgcg	gtatctgcag	tgcggcgggt	cgtaggcggga	ggattgggga	780
cagcttttcgg	ggacggcctt	gacgccccag	ggtgccgagc	cccagagcaa	cgcgggccca	840
cgaccccata	tcggggaaac	gttattttacc	ctgttttcggg	cccccgagtt	gctggccccc	900
aacggcgacc	tgtacaacgt	gtttgccttg	gccttgagc	tcttgccaa	acgcctccgt	960
cccatgcacg	tctttatcct	ggattacgac	caatcgcccg	ccggctgccg	ggacgccctg	1020
ctgcaactta	cctccgggat	ggtccagacc	cacgtcacca	ccccggctc	cataccgacg	1080

sequence listing_ST25.txt

atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 233
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-59

<400> 233
 atggcttcgt accccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc 60
 ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
 cgcccggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg 180
 gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
 gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc 300
 tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggtg 360
 atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
 cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
 ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ctttatgggc 540
 agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc 600
 acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc 660
 cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
 ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
 cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
 cgaccccata tcggggacac gttatttacc ctgtttcggg ccccagatt gctggcccc 900
 aacggcgacc tgtacaacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
 cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgcctg 1020
 ctgcaactta cctccgggat gatccagacc cacgtcacca cccaggctc cataccgacg 1080
 atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 234
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-60

<400> 234
 atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60

sequence listing_ST25.txt

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ggccatagca accgacgtac ggcgttgcg cctcgccggc aacaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccaggtt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgttaccggc ccgcgcgata ctttatgggc 540
agcatgaccc cccaggccgt gctggcggtt gtggccctca tcccgccgac cttgccggc 600
acaaacatcg tgttgggggc ctttcggag gacagacaca ccgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacgag 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtacca ccccggtc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

```

```

<210> 235
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-61

```

```

<400> 235
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc aacaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccaggtt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480

```

sequence listing_ST25.txt

```

ttcgaccgcc atcccatcgc cgccctcctg tgttacccgg ccgcgcgata ctttatgggc 540
agcatgaccc cccaggccgt gctgggtgttc gtggccctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc ctttccggag gacagacaca ccgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacgag 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccagagtt gctggccccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggtgccc ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

```

<210> 236

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-62

<400> 236

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caccgggagc agaaaatgcc cagcgtactg cgggtttata tagacggtcc ccacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
ctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ctttatgggc 540
agcatgaccc cccaggccgt gctggcggtt gtggccctca tcccgccgac cttgcccggc 600
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cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccagagtt gctggccccc 900

```

sequence listing_ST25.txt

aacggcgacc tgtacaacgt gtttgccctgg gccttggacg tcttggccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat gatccagacc cacgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctcac	1128

<210> 237
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-63

<400> 237	
atggcttcgt accccggcca tcaacacgcg tctgcttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cacctggagc agaaaatgcc cacgctactg cgggtttata tagacgggcc tcacgggatg	180
gggaaaacca ccaccacgca actgctgggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc cccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcggta ccttatgggc	540
agcatgaccc cccaggccgt gctggcgctc gtggtcctca tccgcgcgac cttgcccggc	600
acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
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cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
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aacggcgacc tgtacaacgt gtttgccctgg gccttggacg tcttggccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctcac	1128

<210> 238
 <211> 1128
 <212> DNA
 <213> artificial sequence

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-64

<400> 238

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atggcttcgt accccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc      120
cacctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cggaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg      360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggc tgggagctca catgccccgc cccggccct caccctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcggta ccttatgggc      540
agcatgaccc cccaggccgt gctggcggtc gtggtcctca tcccgccgac cttgcccggc      600
acaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg ccgttacggg      720
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cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggccccc      900
aacggcgacc tgtacaacgt gtttgccctg gccttgagc tcttggccaa acgcctccgt      960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggtgccg ggacgccctg     1020
ctgcaactta cctccgggat gatccagacc cacgtcacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                    1128

```

<210> 239

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-65

<400> 239

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ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc      120
cacctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240

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sequence listing_ST25.txt

gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc	300
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atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc	480
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cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggaaac gttatttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtacaacgt gtttgccctg gccttggaagc tcttgcccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctcac	1128

<210> 240
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-66

<400> 240	
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ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcagggt ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttccggag gacagacaca tcgaccgcct ggccaaacgc	660

sequence listing_ST25.txt

cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgga ggattggga	780
cagctttcgg ggacggcgt gccgccccag ggtgccgagc cccagagcaa cgcgggcca	840
cgacccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgcttg gccttgagc tcttgccaa acgcctcgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tgggtgcgac gtttgcccgg gagatggggg aggctaac	1128

<210> 241
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-67

<400> 241	
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ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cacctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atccaatcgc cgccctcctg tgctaccgga ccgcgcggta ccttatgggc	540
agcatgacct cccaggccgt gctggcgctt gtggtcctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc	660
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cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggcca	840
cgacccata tcggggaaac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtacaacgt gtttgcttg gccttgagc tcttgccaa acgcctcgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
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sequence listing_ST25.txt

atctgcgacc tggcgcgcac gtttggccgg gagatggggg aggctcac 1128

<210> 242
<211> 1128
<212> DNA
<213> artificial sequence

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-68

<400> 242
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<210> 243
<211> 1128
<212> DNA
<213> artificial sequence

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-69

<400> 243
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sequence listing_ST25.txt

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<210> 244

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-70

<400> 244

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cgcccggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg 180
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gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc 300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
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sequence_listing_ST25.txt

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cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
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cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggccca	840
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aacggcgacc tgtacaacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggctc cataccgacg	1080
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<210> 245
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-71

<400> 245	
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sequence listing_ST25.txt

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